Search Strategy

FILE 'USPATFULL' ENTERED AT 17:22:41 ON 22 OCT 1999

		E	ALIZON MARC/IN
L1	20	S	E3
		E	SONIGO PIERRE/IN
L2	20	S	E3
L3	2	S	L2 NOT L1
		E	WAIN-HOBSON SIMON/IN
		E	WAIN HOBSON SIMON/IN
L4	10	S	E3
L5	4	S	L4 NOT L1 OR L3
		E	MONTAGNIER LUC/IN
L6	55	S	E3
L7	36	S	L6 NOT (L1 OR L2 OR L4)
L8	8841	S	(HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9	2003	S	L8 AND (VARIANT?)
L10	1183	S	L9 AND (NUCLEOTIDE SEQUENCE?)
L11	41	S	L10 AND (MOLECULAR CLONE?)

FILE 'EUROPATFULL' ENTERED AT 17:42:17 ON 22 OCT 1999

		E	ALIZON MARC/IN
		E	ALIZON M/IN
L12	4	S	E2
		E	SONGIO P/IN
		E	SONIGO/IN
L13	4	S	E3
		E	WAIN-HOBSON/IN
L14	15	S	E2
		E	WAINHOBSON/IN
		E	HOBSON/IN
L15	24	S	E3
		E	MONTAGNIER/IN
L16	30	S	E3
L17	1819	S	(HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L18	437	S	L17 AND (VARIANT?)
L19	246	S	L18 AND (NUCLEOTIDE SEQUENC?)
L20	190	S	L19 AND (MOLECULAR CLON?)

FILE 'AIDSLINE' ENTERED AT 17:45:51 ON 22 OCT 1999

		E	ALIZON MARC/AU
L21	42	S	E2
		E	SONIGO P/AU
L22	59	S	E3
L23	52	S	L22 NOT L21
		E	WAIN-HOBSON S/AU
		E	WAIN HOBSON S/AU
L24	102	S	E3
L25	93	S	L24 NOT (L21 OR L22)
		E	MONTAGNIER LUC/AU
L26	309	S	E1
L27	296	S	L26 NOT (L21 OR L22 OR L24)
L28	39108	S	(HIV-1 OR HUMAN IMMUNODEFICIENCY VIRUS TYPE 1)
L29	1600	S	L28 AND VARIANT?
L30	66	S	L29 AND (NUCLEOTIDE SEQUENC?)

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L31           9 S L30 AND (MOLECULAR CLON?)

     FILE 'USPATFULL' ENTERED AT 19:20:53 ON 22 APR 1998

                 E ALIZON MARC/IN
L1           11 S E3
                 E MONTAGNIER LUC/IN
L2           42 S E3
L3           32 S L2 NOT L1
L4           24 S L3 AND LAV
                 E LUCIW PAUL
                 E LUCIW, PAUL/IN
                 E LUCIW PAUL/IN
L5            4 S E3 OR E4
                 E LEVY JAY/IN
L6            8 S E4

     FILE 'MEDLINE' ENTERED AT 19:39:54 ON 22 APR 1998

                 E ALIZON, M/AU
L7           35 S E2
L8            5 S L7 AND LAV
L9           30 S L7 NOT L8
                 E MONTAGNIER LUC/AU
L10         274 S E2
L11          27 S L10 AND LAV
L12           1 S LAVMAL
L13           1 S LAV AND MAL
                 E HAHN B/AU
L14         161 S E6
L15           8 S L14 AND PY=1985
L16           3 S L14 AND PY=1986
                 E RATNER LEE/AU
                 E RATNER L/AU
L17         125 S E3
                 E GALLO R C/AU

L1   ANSWER 10 OF 11  USPATFULL
91:59054 Variant of LAV viruses.
      ***Alizon, Marc***  , Paris, France
    Sonigo, Pierre, Paris, France
    Wain-Hobson, Simon, Montigny les Bretonneux, France
    Montagnier, Luc, Le Plessis Robinson, France
    Institut Pasteur, Paris, France (non-U.S. corporation)
    US 5034511 910723
    APPLICATION: US 87-38332  870413 (7)
    DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB     A variant of a LAV virus, designated LAV.sub.ELI and capable of
       causing AIDS. The cDNA and antigens of the LAV.sub.ELI virus can
       be used for the diagnosis of AIDS and pre-AIDS.

CLM    What is claimed is:
       1. An isolated or synthetic peptide comprising an amino acid
       sequence that is a fragment of the following amino acid sequence:
       ##STR1## wherein, in said amino acid sequence, A is alanine, C is
       cysteine, D is aspartic acid, E is glutamic acid, F is
       phenylalanine, G is glycine, H is histidine, I is isoleucine, K is
       lysine, L is leucine, M is methionine, N is asparagine, P is
       proline, Q is glutamine, R is arginine, S is serine, T is
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threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, amino-acyl residues 531-877 of an envelope glycoprotein of LAV.sub.ELI virus.

2. An isolated or synthetic peptide as claimed in claim 1, wherein said amino acid sequence comprises a sequence selected from the group consisting of amino-acyl residues 37 to 130, 211 to 289, and 488 to 530.

3. An isolated or synthetic peptide as claimed in claim 1, wherein said amino acid sequence comprises amino-acyl residues 490 to 620 or 680 to 700.

4. An isolated or synthetic peptide as claimed in claim 1, wherein said amino acid sequence comprises a sequence selected from the group consisting of: amino-acyl residues 1 to 530; amino-acyl residues 34 to 530; and amino-acyl residues 531 to 877.

5. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 1, and a physiologically acceptable carrier.

6. A diagnostic kit for the in vitro detection of antibodies against a lymphadenopathy associated virus comprising an isolated or synthetic peptide as claimed in claim 1, and a reagent for detecting the formation of peptide/antibody complex.

7. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p25 peptide comprising amino-acyl residues 138-385 of gag protein of LAV.sub.ELI virus.

8. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p13 peptide comprising amino-acyl residues 385-519 of gag protein of LAV.sub.ELI virus.

9. An isolated or synthetic peptide comprising an amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine.

L1 ANSWER 11 OF 11 USPATFULL
91:54851 Variant of LAV viruses.
Alizon, Marc , Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny Les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5030714 910709
APPLICATION: US 87-38330 870413 (7)
PRIORITY: EP 86-401380 860623
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A variant of the LAV virus, designated LAV.sub.MAL and capable of causing AIDS. The cDNA and antigens of the LAV.sub.MAL virus can be used for the diagnosis of AIDS and pre-AIDS.

CLM What is claimed is:

1. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residue 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, amino-acyl residues 531-877 of an envelope glycoprotein of LAV.sub.MAL virus.

2. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 1 and a physiologically acceptable carrier, wherein said immunogenic composition is capable of eliciting an immune response to said peptide in a host.

3. An immunogenic composition as claimed in claim 2, wherein said peptide is coupled to a physiologically acceptable and non-toxic carrier molecule that is capable of enhancing the immunogenicity of the peptide.

4. An immunogenic composition as claimed in claim 3, wherein said carrier molecule is a natural protein or a synthetic macromolecular carrier.

5. An immunogenic composition as claimed in claim 4, wherein said natural protein is selected from the group consisting of tetanus toxoid, ovalbumin, serum albumin, and hemocyanin.

6. An immunogenic composition as claimed in claim 4, wherein said synthetic macromolecular carrier is polylysine or poly(D-L alanine)-poly(L-lysine).

7. The peptide of claim 1, wherein said peptide is a glycoprotein.

8. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 37-130 of the envelope glycoprotein of LAV.sub.MAL virus.

9. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 211-289 of the envelope glycoprotein of LAV.sub.MAL virus.

10. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 488-530 of the envelope glycoprotein of LAV.sub.MAL virus.

11. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 490-620 of the envelope glycoprotein of LAV.sub.MAL virus.

12. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 680-700 of the envelope glycoprotein of LAV.sub.MAL virus.

13. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 1-530 of the envelope glycoprotein of LAV.sub.MAL virus.

14. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 34-530 of the envelope glycoprotein of LAV.sub.MAL virus.

15. An isolated or synthetic peptide as claimed in claim 1, wherein said fragment comprises amino-acyl residues 531-877 of the envelope glycoprotein of LAV.sub.MAL virus.

16. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p25 peptide comprising amino-acyl residues 138-385 of gag protein of LAV.sub.MAL virus.

17. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 16 and a physiologically acceptable carrier, wherein immunogenic composition is capable of eliciting an immune response to said peptide in a host.

18. An isolated or synthetic peptide comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p13 peptide comprising amino-acyl residues 385-519 of gag protein of LAV.sub.MAL virus.

19. An immunogenic composition comprising an isolated or synthetic peptide as claimed in claim 18 and a physiologically acceptable carrier, wherein immunogenic composition is capable of eliciting an immune response to said peptide in a host.

20. An isolated or synthetic peptide comprising an amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine.

L4 ANSWER 1 OF 24 USPATFULL
97:106928 Nucleotide sequences derived from the genome of retroviruses of the HIV-1, HIV-2 and SIV type, and their uses in particular for the amplification of the genomes of these retroviruses and for the in vitro diagnosis of the disease due to these viruses.
Moncany, Maurice, Paris, France
Montagnier, Luc , Le Plessis-Robinson, France
Institut Pasteur, France (non-U.S. corporation) Institut National de la Sante et de la Recherche Medicale, France (non-U.S. corporation)
US 5688637 971118
APPLICATION: US 93-160465 931202 (8)
PRIORITY: FR 89-7354 890602
FR 89-12371 890920
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to nucleotidic sequences derived from genomes of the HIV-1 type virus, or from genomes of the HIV-2 type virus, or of the SIV type virus, and their applications, especially as oligo-nucleotidic initiators of implementation of an $i (in vitro) method for the diagnosis of the infection of an individual by a virus of the HIV-1 and/or HIV-2 type.

CLM What is claimed is:
1. An oligonucleotide primer, said primer having a nucleotide sequence selected from the following group of nucleotides oriented in the 5'-3' direction: nucleotides 636-653, 854-872, 1369-1388, and 2021-2039 of the gag gene of HIV-1 Bru; nucleotides 900-881, 1385-1369, 1388-1369, and 2039-2021 of a nucleic acid sequence complementary to the gag gene of HIV-1 Bru; nucleotides 635-652, 864-888, 1403-1421, and 2055-2073 of the gag gene of HIV-1 Mal; nucleotides 916-897, 1419-1403, 1421-1403, and 2073-2055 of a nucleic acid sequence complementary to the gag gene of HIV-1 Mal; nucleotides 636-653, 848-872, 1369-1388, and 2024-2042 of the gag gene of HIV-1 Eli; nucleotides 900-881, 1385-1369, 1388-1369, and 2042-2024 of a nucleic acid sequence complementary to the gag gene of HIV-1 Eli; nucleotides 859-876, 1160-1184, 1687-1706, and 2329-2349 of the gag gene of HIV-2 ROD; nucleotides 1212-1193, 1703-1687, 1706-1687, and 2349-2329 of a nucleic acid sequence complementary to the gag gene of HIV-2 ROD; nucleotides 834-851, 1124-1148, 1651-1670, and 2299-2318 of the gag gene of SIV-MAC; and nucleotides 1176-1157, 1667-1651, 1670-1651, and 2318-2299 of a nucleic acid sequence complementary to the gag gene of SIV-MAC; nucleotides 5590-5610 of the vpr gene of HIV-1 Bru; nucleotides 5870-5849 of a nucleic acid sequence complementary to the vpr gene of HIV-1 Bru; nucleotides 5585-5605 of the vpr gene of HIV-1 Mal; nucleotides 5865-5844 of a nucleic acid sequence complementary to the vpr gene of HIV-1 Mal, nucleotides 5554-5574 of the vpr gene of HIV-1 Eli; nucleotides 5834-5813 of a nucleic acid sequence complementary to the vpr gene of HIV-1 Eli; nucleotides 6233-6296 of the vpr gene of HIV-2 ROD; nucleotides 6551-6531 of a nucleic acid sequence complementary to the vpr gene of HIV-2 ROD; nucleotides 6147-6170 of the vpr gene of SIV-MAC; and nucleotides

6454-6431 of a nucleic acid sequence complementary to the vpr gene of SIV-MAC; nucleotides 2620-2643, 3339-3361, 4186-4207, and 4992-5011 of the pol gene of HIV-1 Bru; nucleotides 2643-2620, 3361-3339, 4207-4186, and 5011-4992 of a nucleic acid sequence complementary to the pol gene of HIV-1 Bru; nucleotides 2615-2638, 3333-3356, 4181-4202, and 4987-5006 of the pol gene of HIV-1 Mal; nucleotides 2638-2615, 3356-3334, 4202-4181, and 5006-4987 of a nucleic acid sequence complementary to the pol gene of HIV-1 Mal; nucleotides 2584-2607, 3303-3325, 4150-4171, and 4956-4975 of the pol gene of HIV-1 Eli; nucleotides 2607-2584, 3325-3303, 4171-4150, and 4975-4956 of a nucleic acid sequence complementary to the pol gene of HIV-1 Eli; nucleotides 2971-2994, 3690-3712, 4534-4555, and 5340-5359 of the pol gene of HIV-2 ROD; nucleotides 2994-2971, 3712-3690, 4555-4534, and 5359-5340 of a nucleic acid sequence complementary to the pol gene of HIV-2 ROD; nucleotides 2887-3010, 3606-3628, 4450-4471, and 5275-5256 of a nucleic acid sequence complementory to the pol gene of SIV-MAC; 5256-5275 of the pol gene of SIV-MAC; and nucleotides 3010-2887, 3628-3606, 4471-4450, and nucleotides 9165-9185 and 9542-9564 of the nef2 gene of HIV-2 ROD; 9564-9542 and 9956-9933 of a nucleic acid sequence complementary to the nef2 gene of HIV-2 ROD; nucleotides 9139-9159 and 9516-9538 of the nef2 gene of SIV-MAC; 9538-9516 and 9839-9870 of a nucleic acid sequence complementary to the nef2 gene of SIV-MAC; nucleotides 5424-5450 and 5754-5775 of the vif2 gene of HIV-2 ROD; nucleotides 5775-5754 and 6082-6061 of a nucleic acid sequence complementary to the vif2 gene of HIV-2 ROD; nucleotides 5340-5366 and 5670-5691 of the vif2 gene of HIV-2 ROD; nucleotides 5691-5670 and 5995-5974 of a nucleic acid sequence complementary to the vif2 gene of SIV-MAC; nucleotides 5900-5918 of the vpx gene of HIV-2 ROD; nucleotides 6228-6208 of a nucleic acid sequence complementary to the vpx gene of HIV-2 ROD; nucleotides 5813-5831 of the vpx gene of HIV-2 ROD; nucleotides 6141-6121 of a nucleic acid sequence complementary to the vpx gene of SIV-MAC; nucleotides 6905-6930, 7055-7077, 7360-7384, 7832-7857, 8844-8869, 7629-7647, and 8224-8242 of the env gene of HIV-1 Bru; nucleotides 6930-6905, 7384-7360, 7857-7832, 8869-8844, and 8242-8224 of a nucleic acid sequence complementary to the env gene of HIV-1 Bru; nucleotides 6903-6928, 7053-7075, 7821-7846, 7821-7846, 7612-7630, 8213-8231, and 8836-8861 of the env gene of HIV-1 Mal; nucleotides 6928-6903, 7373-7349, 7846-7821, 8861-8836, and 8231-8213 of a nucleic acid sequence complementary to the env gene of HIV-1 Mal; nucleotides 6860-6885, 7010-7032, 7306-7330, 7775-7800, 8787-8812, 7572-7590, and 8167-8185 of the env gene of HIV-1 Eli; and nucleotides 6885-6860, 7330-7306, 7800-7775, 8812-8787, and 8185-8167 of a nucleic acid sequence complementary to the env gene of HIV-1 Eli; nucleotides 9116-9136 of the nef1 gene of HIV-1 Bru; nucleotides 9136-9116 and 9503-9483 of a nucleic acid sequence complementary to the nef1 gene of HIV-1 Bru; nucleotides 9117-9137 of the nef1 gene of HIV-1 Mal; and nucleotides 9137-9117 and 9505-9484 of a nucleic acid sequence complementary to the nef1 gene of HIV-1 Mal; nucleotides 9062-9082 of the nef1 gene of HIV-Eli; nucleotides 9082-9062 and 9449-9428 of a nucleic acid sequence complementary to the nef1 gene of HIV-1 Eli; nucleotides 5073-5099 and 5383-5405 of the vif1 gene of HIV-1 Bru; and nucleotides 5405-5383 and 5675-5653 of a nucleic acid sequence complementary to the vif1 gene of HIV-1 Bru; nucleotides 5068-5094 and 5378-5400 of the vif1 gene of HIV-1 Mal; nucleotides 5400-5378 and 5670-5648 of a nucleic acid sequence complementary to the vif1 gene of HIV-1 Mal; and nucleotides 5037-5063 and 5347-5369 of the vif1 gene of HIV-1 Eli; nucleotides 5369-5347 and 5639-5617 of a nucleic acid sequence complementary to the vif1

gene of HIV-1 Eli; nucleotides 6081-6105 and 6240-6263 of the vpu gene of HIV-1 Bru; nucleotides 6343-6321 of a nucleic acid sequence complementary to the vpu gene of HIV-1 Bru; nucleotides 6076-6100 and 6238-6261 of the vpu gene of HIV-1 Mal; nucleotides 6338-6316 of a nucleic acid sequence complementary to the vpu gene of HIV-1 Mal; nucleotides 6045-6069 and 6207-6230 of the vpu gene of SIV-MAC; and nucleotides 6307-6285 of a nucleic acid sequence complementary to the vpu gene of SIV-MAC.

2. An oligonucleotide primer selected from the group consisting of primers having the following nucleotide sequences from 5' to 3': MMy1: TGG CGC CCGAAC AGG GAC TGG CGC CTGAAC AGG GAC MMy2: GGC CAG GGG GAAAGAAAAA GGC CCG GCG GAAAGAAAAA MMy3: TGC CCA TACAAAATG TTT TA TGC CCA CAC TAT ATG TTT TA MMy4: TGC ATG GCT GCT TGA TG TGC ATA GCT GCC TGG TG MMy4B: CTT TGC ATG GCT GCT TGA TG CTC TGC ATA GCT GCT TGC TG MMy4Ba: CAT CAAGCA GCC ATG CAAAG CAC CAG GCA GCT ATG CAG AG MMy28: AGG GCT GTT GGAAAT GTG G AGG GCT GTT GGA AGT GTG G MMy28a: CCA CAT TTC CAG CAT CCC T CCA CAT TTC CAG CAG CCC T CCA CAT TTC CAG CAC CCC T MMy18: GAT AGA TGGAAC AAG CCC CAG MMy19: TCC ATT TCT TGC TCT CCT CTG T MMy29: TAAAGC CAG GAA TGG ATG GCC CAA TAAAGC CAG GAA TGG ATG GAC CAA MMy29a: TTG GGC CAT CCA TTC CTG GCT TTA TTG GTC CAT CCA TTC CTG GCT TTA MMy30: TGG ACT GTC AAT GAC ATA CAGAA TGG ACT GTC AAT GAT ATA CAGAA MMy30a: TTC TGT ATG TCA TTG ACA GTC CA TTC TGT ATG TCA TTG ACT GTC CA MMy31: CAT GGG TAC CAG CAC ACAAAG G MMy31a: CCT TTG TGT GCT GGT ACC CAT G MMy32: TGG AAA GGT GAA GGG GCA GT TGG AAA GGT GAAGGA GCA GT MMy32a: ACT GCC CCT TCA CCT TTC CA ACT GCC CCT TCT CCT TTC CA ACT GCC CCT TCC CCT TTC CA MMy12: AGA GAC TCT TGC GGG CGC GTG MMy13: ATA TAC TTA GAAAAG GAA GAAGG MMy13a: CCT TCT TCC TTT TCTAAG TAT AT MMy14: AGC TGA GAC AGC AGG GAC TTT CCA MMy20: TAT GGA GGA GGAAAAGAG ATG GAT AGT MMy21: TAG CAC TTA TTT CCC TTG CTT T MMy21a: AAA GCA AGG GAAATA AGT GCT A MMY22: CCC TTG TTC ATC ATG CCA GTA T MMy23: ATG TCA GAT CCC AGG GAG A MMy24: CCT GGA GGG GGA GGA GGA GGA MMy5: CCA ATT CCC ATA CAT TAT TGT GCC CC MMy5a: GGG GCA CAA TAATGT ATG GGA ATT GG MMy6: AAT GGC AGT CTA GCA GAA GAA GA MMy7: ATC CTC A0G AGG GGA CCC AGAAAT T MMy7a: AAT TTC TGG GTC CCC TCC TGA GGA T MMy8a: GTG CTT CCT GCT GCT CCC AAG AAC CC MMy8a: GGG TTC TTG GGA GCA GCA GGA AGC AC MMy9: ATG GGT GGC AAG TGG TCAAAAAGT AG ATG GGT GGCAAATGG TCAAAAAGT AG MMy9a: CTA CTT TTT GAC CAC TTG CCA CCC AT MMy89: TTC ATT CTT TTC TTG CTG G MMy10: AAAAGAAAAGGG GGG ACT GGA MMy10a: TCC AGT CCC CCC TTT TCT TTT MMy11: AAA GTC CCC AGC GGAAAG TCC C MMy15: GAT TAT GGAAAA CAG ATG GCA GGT GAT MMy16: GCAGAC CAACTA ATT CAT CTG TA MMy16a: TAC AGA TGA ATT AGT TGG TCT GC MMy17: CTT AAG CTC CTC TAAAAG CTC TA MMy25: GTA AGT AGT ACA TGTAAT GCA ACC T MMy26: AGC AGA AGA CAG TGG CCATGA GAG MMy27: ACT ACA GAT CAT CAATAT CCC AA.

3. A method for amplifying nucleic acids of viruses of the HIV-1, HIV-2, and SIV type in a biological sample, said method comprising a) extracting said nucleic acid from said biological sample; b) treating said nucleic acid with a reverse transcriptase if said nucleic acid is RNA; and c) performing an amplification cycle comprising the following steps: denaturing the nucleic acid to be detected to form single-stranded nucleic acids, hybridizing each of said nucleic acid single strands with at least one primer according to any one of claims 1 and 2, by placing said single strands in contact with at least one of said primers, and amplifying said nucleic acid strands by elongation of said primers along the strands to which they are hybridized in the presence of a polymerase, dATP, dGTP, dCTP and dTTP, said cycle being repeated about 30 to about 40 times.

4. The method of claim 3 wherein the step of denaturing the nucleic acid is carried out in the presence of said primer.

5. A method of in vitro diagnosis of infection of a mammal by a virus selected from the group consisting of HIV-1, HIV-2, and SIV, said method comprising detecting nucleic acid of said virus by a) obtaining a biological sample from said mammal, wherein said biological sample comprises nucleic acid; b) extracting nucleic acid of said virus from said biological sample and, if said nucleic acid is RNA, treating said nucleic acid with a reverse transcriptase to produce a double-stranded nucleic acid comprising said nucleic acid and its complementary strand; c) performing an amplification cycle comprising the following steps: denaturing the double-stranded nucleic acid to be detected to form single-stranded nucleic acids, hybridizing each of said nucleic acid single strands with at least one primer according to any one of claims 1 and 2, by placing said single strand in contact with said primer under hybridization conditions, and amplifying said nucleic acid single strands by elongation of said primers along the strands to which they are hybridized in the presence of a polymerase, dATP, dGTP, dCTP and dTTP, said cycle being repeated about 10 to about 60 times; d) detecting the nucleic acid of said virus and e) correlating the presence of the nucleic acid of said virus with infection by said virus.

6. The diagnostic method of claim 5, wherein the hybridization step of the cycle is carried out by placing each of said single-stranded nucleic acids in contact with said primers, wherein said primers hybridize with a nucleotide sequence situated on the first strand of said double-stranded nucleic acid and with a nucleotide sequence situated on the strand complementary to said first strand, said nucleic acid sequences being separated by a region of about 50 to about 10,000 base pairs when said complementary strands are hybridized to form one double-stranded nucleic acid.

7. The method of claim 6, wherein said region is about 100 to about 1100 base pairs.

8. The method according to claim 5, wherein said detecting step (d) comprises hybridizing at least one detectably labelled nucleotide probe to said amplified nucleic acid.

9. The method of claim 5 wherein said virus is HIV-1 or HIV-2, and said primer couple is selected from the group consisting of MMy1-MMy4, MMy2-MMy4, MMy1-MMy3, MMy18-MMy19, MMy4a-MMy28a, MMy28-MMy29a, MMy29-MMy30a, and MMy31-MMy32a.

10. The method of claim 5 wherein said virus is HIV-1, and said primer couple is selected from the group consisting of MMy5-MMy8, MMy6-MMy8, MMy7-MMy8, MMy5-MMy7a, MMy6-MMy7a, MMy9-MMy11, MMy10-MMy11, MMy9-MMy10a, MMy26-MMy5a, MMy8a-MMy9a, MMy8a-MMy89a, MMy89a-MMy9a, MMy15-MMy17, MMy15-MMy16a, MMy16-MMy17, MMy25-MMy27, and MMy26-MMy27.

11. The method of claim 5, wherein said virus is HIV-2, and said primer, couple is selected from the group consisting of MMy20-MMy22, MMy20,-MMy21a, MMy21-MMy22, MMy23-MMy24, MMy12-MMy14, and MMy12 MMy13a.

12. The method of claim 5, wherein said virus comprises a gene selected from the group consisting of gag, vpr, env, nef1, vif1, vif2, vpx, nef2, vpu and pol, and said primer couple is selected from the group consisting of MMy1-MMy4, MMy2-MMy4, MMy1-MMy3, MMy4a-MMy28a for the gag gene; MMy18-MMy19 for the vpr gene; MMy5-MMy8, MMy6-MMy8, MMy7-MMy8, MMy5-MMy7a, MMy6-MMy7a, MMy26-MMy5a, MMy8a-MMy9a, MMy8a-MMy89, MMy89a-MMy9a for the env gene; MMy9-MMy11, MMy9-MMy10a, MMy10-MMy11 for the nef1 gene; MMy15-MMy17, MMy15-MMy16a, MMy16-MMy17 for the vif1 gene; MMy20-MMy22, MMy20-MMy21a, MMy21-MMy22 for the vif2 gene; MMy23-MMy24 for the vpx gene; MMy12-MMy14, MMy12-MMy13a, MMy13-MMy14 for the nef2 gene; MMy25-MMy27, MMy26-MMy27 for the vpu gene; and MMy28-MMy29a, MMy29-MMy30a, MMy30-MMy31a, MMy31-MMy32a for the pol gene.

13. A diagnostic kit for the in vitro diagnosis of infection of a meal by a virus selected from the group consisting of HIV-1, HIV-2, and SIV by detecting the presence of HIV-1, HIV-2 or SIV nucleic acid or a strand of DNA complementary to said nucleic acid, said kit comprising a) at least a first and a second prime according to any one of claims 1 and 2, wherein said first primer is complementary to a region of nucleotides of the nucleic acid of said virus, and said second primer is complementary to a region of nucleotides of the strand of DNA complementary to said nucleic acid of said virus, wherein said regions of nucleotides are separated by about 50 to about 10,000 base pairs when said complementary strands are incorporated into one double-stranded nucleic acid; b) reagents for amplifying said nucleic acid; and c) at least one detectably labelled probe capable of hybridizing with the amplified nucleotide sequence to be detected.

14. An oligonucleotide primer couple for the amplification according to any one of claims 3 and 5, said primer couple selected from the group consisting of MMy4Ba-MMy28a, MMy26-MMy5a, MMy8a-MMy89, MMy89a-MMy9a, MMy25-MMy27, MMy26-MMy27, MMy28-MMy29a, MMy29-MM30a, MMy30-MMy31a, and MMy31-MMy32a.

L4 ANSWER 17 OF 24 USPATFULL
92:100919 Viral vector coding glycoprotein of HIV-1.
Kieny, Marie-Paule, Strasbourg, France
Rautmann, Guy, Strasbourg, France
Lecocq, Jean-Pierre, Reichstett, France
Hobson, Simon W., Montigny-le-Bretonneux, France
Girard, Marc, Paris, France
Montagnier, Luc , Le Plessis-Robinson, France
Transgene S.A., Institut Pasteur, France (non-U.S. corporation)
US 5169763 921208
APPLICATION: US 91-765413 910924 (7)
PRIORITY: FR 86-5043 860408
FR 86-15106 861029
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A viral vector comprising at least a portion of the genome of the HIV virus, a gene coding gp160 glycoprotein of the envelope of the HIV virus, as well as the elements providing for the expression of the glycoprotein in cells, wherein the gp160 is expressed as a non-cleavable protein.

CLM What is claimed is:
1. A viral vector, the genome of which comprises: a functional

origin of replication of a poxvirus; a first DNA fragment encoding a non-cleavable gp160, consisting of gp120-gp140, derived from the natural gp160 of an HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequence REKR originally found in the natural gp160; a second DNA fragment encoding a signal peptide, said second DNA fragment being linked to the 5' end of said first DNA fragment; and a promoter for expressing said DNA fragment in mammalian cells.

2. A viral vector according to claim 1, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequences KRR and REKR originally found in the natural gp160.

3. A viral vector according to claim 1, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160.

4. A viral vector according to claim 2, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160, and in that it comprises a 3-amino acid sequence other than KRR in place of the amino acid sequence KRR originally found in the natural gp160.

5. A viral vector according to claim 3, the genome of which comprises a DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being different from the natural gp160 in that the amino acid sequence REKR originally found in the natural gp160 is replaced by the amino acid sequence NEHQ.

6. A viral vector according to claim 4, the genome of which comprises a DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being different from the natural gp160 in that the amino acid sequences KRR and REKR are replaced respectively by the amino acid sequences QNH and NEHQ.

7. A viral vector according to claim 1, the genome of which comprises a first DNA fragment encoding a non-cleavable and soluble gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable and soluble gp160 being different from the natural gp160 in that it does not contain the amino acid sequence REKR originally found in the natural gp160, and in that the transmembrane region originally found in the natural gp160 is deleted.

8. A viral vector according to claim 7, wherein said non-cleavable and soluble gp160 is different from the natural gp160 in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160.

9. A viral vector according to claim 8, wherein said non-cleavable

and soluble gp160 is different from the natural gp160 in that the amino acid sequence REKR originally found in the natural gp160 is replaced by the amino acid sequence NEHQ.

10. A viral vector according to claim 2, the genome of which comprises a first DNA fragment encoding a non-cleavable and soluble gp160 derived form the natural gp160 of the HIV-1 virus, said non-cleavable and soluble gp160 being different from the natural gp160 in that it does not contain the amino acid sequences KRR and REKR originally found in the natural gp160, and in that the transmembrane region originally found in the natural gp160 is deleted.

11. A viral vector according to claim 10, wherein said non-cleavable and soluble gp160 is different from the natural gp160 in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160, and a 3-amino acid sequence other than KRR in place of the amino acid sequence KRR originally found in the natural gp160.

12. A viral vector according to claim 11, wherein said non-cleavable and soluble gp160 is different from the natural gp160 in that the amino acid sequences KRR and REKR are replaced respectively by the amino acid sequences QNH and NEHQ.

13. A viral vector according to claim 1, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived form the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequence REKR originally found in the natural gp160, and in that the transmembrane region originally found in the natural gp160 is replaced by the transmembrane region of the glycoprotein of the rabies virus.

14. A viral vector according to claim 13, wherein said non-cleavable gp160 is characterized in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160.

15. A viral vector according to claim 2, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequences KRR and REKR originally found in the natural gp160, and in that the transmembrane region originally found in the natural gp160 is replaced by the transmembrane region of the glycoprotein of the rabies virus.

16. A viral vector according to claim 15, wherein said non-cleavable gp160 is characterized in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160, and a 3-amino acid sequence other than KRR in place of the amino acid sequence KRR originally found in the natural gp160.

17. A viral vector according to claim 1, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequence REKR originally found in the

natural gp160, and in that the amino acid Arg of the transmembrane region originally found in the natural gp160 is replaced by the amino acid Ile.

18. A viral vector according to claim 17, wherein said non-cleavable gp160 is characterized in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160.

19. A viral vector according to claim 2, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequences KRR and REKR originally found in the natural gp160, and in that the amino acid Arg of the transmembrane region originally found in the natural gp160 is replaced by the amino acid Ile.

20. A viral vector according to claim 19, wherein said non-cleavable gp160 is characterized in that it comprises a 4-amino acid sequence other than REKR in place of the amino acid sequence REKR originally found in the natural gp160, and a 3-amino acid sequence other than KRR in place of the amino acid sequence KRR originally found in the natural gp160.

21. A viral vector according to claim 1, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequence REKR originally found in the natural gp160, and in that the hydrophobic region proximate to the C-terminal end of the REKR sequence as originally found in the natural gp160 is deleted.

22. A viral vector according to claim 2, the genome of which comprises a first DNA fragment encoding a non-cleavable gp160 derived from the natural gp160 of the HIV-1 virus, said non-cleavable gp160 being characterized in that it does not contain the amino acid sequences REKR and KRR originally found in the natural gp160, and in that the hydrophobic region proximate to the C-terminal end of the REKR sequence as originally found in the natural gp160 is deleted.

23. A viral vector according to claim 1, the genome of which comprises a second DNA fragment encoding a signal peptide which is selected from the group consisting of the signal peptide of the precursor of the gp160 of the HIV-1 virus and the signal peptide of the precursor of the glycoprotein of the rabies virus.

24. A viral vector according to claim 2, the genome of which comprises a second DNA fragment encoding a signal peptide which is selected from the group consisting of the signal peptide of the precursor of the gp160 of the HIV-1 virus and the signal peptide of the precursor of the glycoprotein of the rabies virus.

25. A viral vector according to claim 1, the genome of which comprises a functional origin of replication of a poxvirus.

26. A viral vector according to claim 25, the genome of which comprises a functional origin of replication of a vaccinia virus.

27. A viral vector according to claim 2, the genome of which comprises a functional origin of replication of a poxvirus.

28. A viral vector according to claim 27, the genome of which comprises a functional origin of replication of a vaccinia virus.

29. A viral vector according to claim 1, wherein the DNA encoding envelope protein of HIV-1 is encoded by the EcoRI-KpnI and KpnI-HindIII fragments of plasmid PJ19-13, comprising nucleotides 1258 to 1698 of the DNA encoding envelope protein of HIV-1, and the HindIII-XhoI fragment of plasmid PJ19-6, comprising nucleotides 1698 to 9173 of the DNA encoding envelope protein of HIV-1.

30. A viral vector according to claim 2, wherein the DNA encoding envelope protein of HIV-1 is encoded by the EcoRI-KpnI and KpnI-HindIII fragments of plasmid PJ19-13, comprising nucleotides 1258 to 1698 of the DNA encoding envelope protein of HIV-1, and the HindIII-XhoI fragment of plasmid PJ19-6, comprising nucleotides 1698 to 9173 of the DNA encoding envelope protein of HIV-1.

31. A culture of mammalian cells, which is infected with a viral vector as claimed in any one of claims 1 to 6 or 13 to 28.

32. A culture of mammalian cells, which is infected with a viral vector as claimed in any one of claims 7 to 12.

33. A process for producing a non-cleavable and soluble gp160 which comprises recovering said non-cleavable gp160 from a culture of mammalian cells as claimed in claim 32.

L5 ANSWER 2 OF 4 USPATFULL
92:86879 Immunoassays for antibody to human immunodeficiency virus using recombinant antigens.
Luciw, Paul A. , Davis, CA, United States
Dina, Dino, San Francisco, CA, United States
Chiron Corporation, Emeryville, CA, United States (U.S. corporation)
US 5156949 921020
APPLICATION: US 87-138894 871224 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Polynucleotide sequences are provided for the diagnosis of the presence of retroviral infection in a human host associated with lymphadenopathy syndrome and/or acquired immune deficiency syndrome, for expression of polypeptides and use of the polypeptides to prepare antibodies, where both the polypeptides and antibodies may be employed as diagnostic reagents or in therapy, e.g., vaccines and passive immunization. The sequences provide detection of the viral infectious agents associated with the indicated syndromes and can be used for expression of antigenic polypeptides.

L8 ANSWER 5 OF 5 MEDLINE
85086249 Document Number: 85086249. Molecular cloning of lymphadenopathy-associated virus. ***Alizon M*** ; Sonigo P; Barre-Sinoussi F; Chermann J C; Tiollais P; Montagnier L; Wain-Hobson S. NATURE, (1984 Dec 20-1985 Jan 2) 312 (5996) 757-60. Journal code: NSC. ISSN: 0028-0836. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Lymphadenopathy-associated virus (***LAV***) is a human retrovirus first isolated from a homosexual patient with lymphadenopathy syndrome, frequently a prodrome or a benign form of acquired immune deficiency syndrome (AIDS). Other ***LAV*** isolates have subsequently been recovered from patients with AIDS or pre-AIDS and all available data are consistent with the virus being the causative agent of AIDS. The virus is propagated on activated T lymphocytes and has a tropism for the T-cell subset OKT4 (ref. 6), in which it induces a cytopathic effect. The major core protein of ***LAV*** is antigenically unrelated to other known retroviral antigens. ***LAV*** -like viruses have more recently been independently isolated from patients with AIDS and pre-AIDS. These viruses, called human T-cell leukaemia/lymphoma virus type III (HTLV-III) and AIDS-associated retrovirus (ARV), seem to have many characteristics in common with ***LAV*** and probably represent independent isolates of the ***LAV*** prototype. We have sought to characterize ***LAV*** by the molecular cloning of its genome. A cloned ***LAV*** complementary DNA was used to screen a library of recombinant phages constructed from the genomic DNA of ***LAV*** -infected T lymphocytes. Two families of clones were characterized which differ in a restriction site. The viral genome is longer than any other human retroviral genome (9.1-9.2

L8 ANSWER 4 OF 5 MEDLINE
85099333 Document Number: 85099333. Nucleotide sequence of the AIDS virus, ***LAV*** . Wain-Hobson S; Sonigo P; Danos O; Cole S; ***Alizon M*** . CELL, (1985 Jan) 40 (1) 9-17. Journal code: CQ4. ISSN: 0092-8674. Pub. country: United States. Language: English.

AB The complete 9193-nucleotide sequence of the probable causative agent of AIDS, lymphadenopathy-associated virus (***LAV***), has been determined. The deduced genetic structure is unique: it shows, in addition to the retroviral gag, pol, and env genes, two novel open reading frames we call Q and F. Remarkably, Q is located between pol and env and F is half-encoded by the U3 element of the LTR. These data place ***LAV*** apart from the previously characterized family of human T cell leukemia/lymphoma viruses.

L8 ANSWER 2 OF 5 MEDLINE
86294252 Document Number: 86294252. Lymphadenopathy/AIDS virus: genetic organization and relationship to animal lentiviruses. ***Alizon M*** ; Montagnier L. ANTICANCER RESEARCH, (1986 May-Jun) 6 (3 Pt B) 403-11. Journal code: 59L. ISSN: 0250-7005. Pub. country: Greece. Language: English.

AB This article presents data obtained by our group in the molecular characterization of the probable agent of the acquired immune deficiency syndrome (AIDS), the lymphadenopathy/AIDS virus (***LAV***). Molecular cloning and complete nucleotide sequencing of ***LAV*** allows a detailed comparison with other AIDS virus isolates, as well as other human and animal retroviruses. We have now molecular evidence that the AIDS virus is closely related to visna virus, prototype of the lentiviruses, whereas the other human retroviruses, i.e., human T-cell leukemia viruses type I and II (HTLV-I and II), are quite remote in the evolution.

L9 ANSWER 25 OF 30 MEDLINE
86245056 Document Number: 86245056. Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients. ***Alizon M*** ; Wain-Hobson S; Montagnier L; Sonigo P. CELL, (1986 Jul 4) 46 (1) 63-74. Journal code: CQ4. ISSN:

0092-8674. Pub. country: United States. Language: English.

AB To define further the genetic variability of the human AIDS retrovirus, we have cloned and sequenced the complete genomes of two isolates obtained from Zairian patients. Their genetic organization is identical with that of isolates from Europe and North America, confirming a common evolutionary origin. However, the comparison of homologous proteins from these different isolates reveals a much greater extent of genetic polymorphism than previously observed. It is nevertheless possible to define conserved domains in the viral proteins, especially in the envelope, that could be of interest for the understanding of the molecular mechanisms of viral pathogenicity and for the development of diagnostic and therapeutic reagents.

L15 ANSWER 4 OF 8 MEDLINE
85270417 Document Number: 85270417. Genomic diversity of the acquired immune deficiency syndrome virus HTLV-III: different viruses exhibit greatest divergence in their envelope genes. ***Hahn B H*** ; Gonda M A; Shaw G M; Popovic M; Hoxie J A; Gallo R C; Wong-Staal F. PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, ***(1985 Jul)*** 82 (14) 4813-7. Journal code: PV3. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB Converging lines of research have linked human T-cell lymphotropic virus type III (HTLV-III) to the pathogenesis of the acquired immune deficiency syndrome. A characteristic feature of this virus is its genomic heterogeneity, which occurs to varying degrees in different viral isolates. To define further the nature and extent of these genomic changes, we compared the molecularly cloned genomes of two variant HTLV-III isolates by extensive restriction enzyme mapping and heteroduplex thermal melt analysis. Both viral isolates were found to be highly related to each other throughout their entire genomic complement, yet they differed markedly in their restriction enzyme maps. Electron microscopic heteroduplex analysis revealed several distinct regions of divergence located almost exclusively in the part of the genome that encodes the viral envelope gene. In vitro culture of one of these viruses over a period of 3 months did not result in any genomic changes as determined by restriction analysis of viral DNA. These results, as well as the recently published nucleotide sequences of other HTLV-III isolates, indicate that the most substantial variation among HTLV-III isolates is located in the envelope. These findings raise the possibility that viral isolates from different individuals could have important biological differences in their envelope antigens, a consideration relevant to ongoing attempts to develop a vaccine against HTLV-III.

L15 ANSWER 2 OF 8 MEDLINE
85272575 Document Number: 85272575. Genomic diversity of human T-lymphotropic virus type III (HTLV-III). Wong-Staal F; Shaw G M; ***Hahn B H*** ; Salahuddin S Z; Popovic M; Markham P; Redfield R; Gallo R C. SCIENCE, ***(1985 Aug 23)*** 229 (4715) 759-62. Journal code: UJ7. ISSN: 0036-8075. Pub. country: United States. Language: English.

AB The DNA genomes of human T-lymphotropic virus type III (HTLV-III) isolated from 18 individuals with AIDS or who were at risk for AIDS were evaluated for evidence of variation. Although all of the 18 viral DNA's hybridized throughout their entire genomes to a full-length cloned probe of the original HTLV-III isolate, each of the 18 isolates showed a different restriction enzyme pattern. The number of restriction site differences between isolates ranged from

only 1 site in 23 to at least 16 sites in 31. No particular viral genotype was associated with a particular disease state and 2 of the 18 patients had evidence of concurrent infection by more than one viral genotype. Propagation of three different viral isolates in vitro for up to 9 months did not lead to detectable changes in their restriction patterns. These findings indicate that different isolates of HTLV-III comprise a spectrum of highly related but distinguishable viruses and have important implications regarding the pathogenicity of HTLV-III and attempts to develop effective diagnostic, therapeutic, and preventive measures for this virus.

L16 ANSWER 3 OF 3 MEDLINE
86218077 Document Number: 86218077. Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS. Starcich B R; ***Hahn B H*** ; Shaw G M; McNeely P D; Modrow S; Wolf H; Parks E S; Parks W P; Josephs S F; Gallo R C; et al. CELL, ***(1986 Jun*** *** 6)*** 45 (5) 637-48. Journal code: CQ4. ISSN: 0092-8674. Pub. country: United States. Language: English.

AB To determine the extent and nature of genetic variation present in independent isolates of HTLV-III/LAV, the nucleotide sequences of the entire envelope gene and parts of gag and pol were determined for two AIDS viruses. The results indicated that variation throughout the viral genome is extensive and that the envelope gene in particular is most highly variable. Within the envelope, changes were most prevalent within the extracellular region where clustered nucleotide substitutions and deletions/insertions were evident. Based on predicted secondary protein structure and hydrophilicity, these hypervariable regions represent potential antigenic sites. In contrast to the hypervariable regions, other sequences in the extracellular envelope and the overall envelope structure (including 18 of 18 cysteine residues), as well as most of the transmembrane region, were highly conserved.

L16 ANSWER 2 OF 3 MEDLINE
86235450 Document Number: 86235450. Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS. ***Hahn B*** *** H*** ; Shaw G M; Taylor M E; Redfield R R; Markham P D; Salahuddin S Z; Wong-Staal F; Gallo R C; Parks E S; Parks W P. SCIENCE, ***(1986 Jun 20)*** 232 (4757) 1548-53. Journal code: UJ7. ISSN: 0036-8075. Pub. country: United States. Language: English.

AB In a study of genetic variation in the AIDS virus, HTLV-III/LAV, sequential virus isolates from persistently infected individuals were examined by Southern blot genomic analysis, molecular cloning, and nucleotide sequencing. Four to six virus isolates were obtained from each of three individuals over a 1-year or 2-year period. Changes were detected throughout the viral genomes and consisted of isolated and clustered nucleotide point mutations as well as short deletions or insertions. Results from genomic restriction mapping and nucleotide sequence comparisons indicated that viruses isolated sequentially had evolved in parallel from a common progenitor virus. The rate of evolution of HTLV-III/LAV was estimated to be at least 10(-3) nucleotide substitutions per site per year for the env gene and 10(-4) for the gag gene, values a millionfold greater than for most DNA genomes. Despite this relatively rapid rate of sequence divergence, virus isolates from any one patient were all much more related to each other than to viruses from other individuals. In view of the substantial heterogeneity among most independent HTLV-III/LAV isolates, the repeated isolation from a given

individual of only highly related viruses raises the possibility that some type of interference mechanism may prevent simultaneous infection by more than one major genotypic form of the virus.

L17 ANSWER 103 OF 125 MEDLINE
86098667 Document Number: 86098667. Transactivation induced by human T-lymphotropic virus type III (HTLV III) maps to a viral sequence encoding 58 amino acids and lacks tissue specificity. Seigel L J; ***Ratner L*** ; Josephs S F; Derse D; Feinberg M B; Reyes G R; O'Brien S J; Wong-Staal F. VIROLOGY, (1986 Jan 15) 148 (1) 226-31. Journal code: XEA. ISSN: 0042-6822. Pub. country: United States. Language: English.

L17 ANSWER 107 OF 125 MEDLINE
85268015 Document Number: 85268015. A molecular clone of HTLV-III with biological activity. Fisher A G; Collalti E; ***Ratner L*** ; Gallo R C; Wong-Staal F. NATURE, (1985 Jul 18-24) 316 (6025) 262-5. Journal code: NSC. ISSN: 0028-0836. Pub. country: ENGLAND: United Kingdom. Language: English.

L17 ANSWER 108 OF 125 MEDLINE
85254466 Document Number: 85254466. Molecular biology of human T-lymphotropic retroviruses. Wong-Staal F; ***Ratner L*** ; Shaw G; Hahn B; Harper M; Franchini G; Gallo R. CANCER RESEARCH, (1985 Sep) 45 (9 Suppl) 4539s-4544s. Ref: 52. Journal code: CNF. ISSN: 0008-5472. Pub. country: United States. Language: English.

L17 ANSWER 92 OF 125 MEDLINE
87299196 Document Number: 87299196. Complete nucleotide sequences of functional clones of the AIDS virus. ***Ratner L*** ; Fisher A; Jagodzinski L L; Mitsuya H; Liou R S; Gallo R C; Wong-Staal F. AIDS RESEARCH AND HUMAN RETROVIRUSES, (1987 Spring) 3 (1) 57-69. Journal code: ART. ISSN: 0889-2229. Pub. country: United States. Language: English.

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    jj                              kkk        ii
                                    kk
    jj  pp ppp    aaaa    rr rrr    kk  kk  iii     nnnnn
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22  22    66      22  22
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  222    66666      222
 22      66  66    22
22  22   66  66   22  22
222222    6666    222222
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5/16/00

L4 ANSWER 23 OF 23 USPATFULL
91:54851 Variant of ***LAV*** viruses.
Alizon, Marc , Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny Les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5030714 19910709
APPLICATION: US 1987-38330 19870413 (7)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A variant of the ***LAV*** virus, designated ***LAV*** .sub.MAL and capable of causing ***AIDS*** . The cDNA and antigens of the ***LAV*** .sub.MAL virus can be used for the diagnosis of ***AIDS*** and pre- ***AIDS*** .
CLM What is claimed is:
1. An isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residue 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, amino-acyl residues 531-877 of an ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

2. An immunogenic composition comprising an isolated or synthetic ***peptide*** as claimed in claim 1 and a physiologically acceptable carrier, wherein said immunogenic composition is capable of eliciting an immune response to said ***peptide*** in a host.

3. An immunogenic composition as claimed in claim 2, wherein said ***peptide*** is coupled to a physiologically acceptable and non-toxic carrier molecule that is capable of enhancing the immunogenicity of the ***peptide*** .

4. An immunogenic composition as claimed in claim 3, wherein said carrier molecule is a natural protein or a synthetic macromolecular carrier.

5. An immunogenic composition as claimed in claim 4, wherein said natural protein is selected from the group consisting of tetanus toxoid, ovalbumin, serum albumin, and hemocyanin.

6. An immunogenic composition as claimed in claim 4, wherein said synthetic macromolecular carrier is polylysine or poly(D-L alanine)-poly(L-lysine).

7. The ***peptide*** of claim 1, wherein said ***peptide*** is a glycoprotein.

8. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 37-130 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

9. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 211-289 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

10. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 488-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

11. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 490-620 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

12. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 680-700 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

13. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 1-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

14. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 34-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

15. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said fragment comprises amino-acyl residues 531-877 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL virus.

16. An isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p25 ***peptide*** comprising amino-acyl residues 138-385 of gag protein of ***LAV*** .sub.MAL virus.

17. An immunogenic composition comprising an isolated or synthetic ***peptide*** as claimed in claim 16 and a physiologically acceptable carrier, wherein immunogenic composition is capable of eliciting an immune response to said ***peptide*** in a host.

18. An isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p13 ***peptide*** comprising amino-acyl residues 385-519 of gag protein of ***LAV*** .sub.MAL virus.

19. An immunogenic composition comprising an isolated or synthetic ***peptide*** as claimed in claim 18 and a physiologically acceptable carrier, wherein immunogenic composition is capable of eliciting an immune response to said ***peptide*** in a host.

20. An isolated or synthetic ***peptide*** comprising an amino acid

sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine.

L4 ANSWER 22 OF 23 USPATFULL
91:59054 Variant of ***LAV*** viruses.
Alizon, Marc , Paris, France
Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5034511 19910723
APPLICATION: US 1987-38332 19870413 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A variant of a ***LAV*** virus, designated ***LAV*** .sub.ELI and capable of causing ***AIDS*** . The cDNA and antigens of the ***LAV*** .sub.ELI virus can be used for the diagnosis of ***AIDS*** and pre- ***AIDS*** .
CLM What is claimed is:
1. An isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, amino-acyl residues 531-877 of an ***envelope*** glycoprotein of ***LAV*** .sub.ELI virus.

2. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said amino acid sequence comprises a sequence selected from the group consisting of amino-acyl residues 37 to 130, 211 to 289, and 488 to 530.

3. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said amino acid sequence comprises amino-acyl residues 490 to 620 or 680 to 700.

4. An isolated or synthetic ***peptide*** as claimed in claim 1, wherein said amino acid sequence comprises a sequence selected from the group consisting of: amino-acyl residues 1 to 530; amino-acyl residues 34 to 530; and amino-acyl residues 531 to 877.

5. An immunogenic composition comprising an isolated or synthetic ***peptide*** as claimed in claim 1, and a physiologically acceptable carrier.

6. A diagnostic kit for the in vitro detection of antibodies against a lymphadenopathy associated virus comprising an isolated or synthetic ***peptide*** as claimed in claim 1, and a reagent for detecting the formation of ***peptide*** /antibody complex.

7. An isolated or synthetic ***peptide*** comprising an amino acid

sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p25 ***peptide*** comprising amino-acyl residues 138-385 of gag protein of ***LAV*** .sub.ELI virus.

8. An isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, and wherein said fragment comprises a p13 ***peptide*** comprising amino-acyl residues 385-519 of gag protein of ***LAV*** .sub.ELI virus.

9. An isolated or synthetic ***peptide*** comprising an amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine.

L4 ANSWER 21 OF 23 USPATFULL
91:77840 ***Peptides*** related to human immunodeficiency virus II (***HIV*** -2).
Alizon, Marc , Paris, France
Montagnier, Luc, Le Plessy Robinson, France
Guetard, Denise, Paris, France
Clavel, Francois, Rockville, MD, United States
Sonigo, Pierre, Paris, France
Guyader, Mireille, Paris, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5051496 19910924
APPLICATION: US 1987-3764 19870116 (7)
PRIORITY: FR 1986-910 19860122
FR 1986-911 19860122
FR 1986-1635 19860206
FR 1986-1985 19860213
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for diagnosing an ***HIV*** -2 (***LAV*** -II) infection and a kit containing reagents for the same is disclosed. These reagents include cDNA probes which are capable of hybridizing to at least a portion of the genome of ***HIV*** -2. In one embodiment, the DNA probes are capable of hybridizing to the entire genome of ***HIV*** -2. These reagents also include polypeptides encoded by some of these DNA sequences.
CLM What is claimed is:
1. A ***peptide*** selecdted from the group consisting of env1, env2, env3, env4, env5, env6, env7, env8, env9, env10, env11 and gag1 of ***HIV*** -2, wherein said ***peptide*** comprises an amino acid sequence that is encoded by a DNA fragment comprising a nucleotide sequence as follows: ##STR3##

2. The ***peptide*** as claimed in claim 1, which is env1.

3. The ***peptide*** as claimed in claim 1, which is env2.

4. The ***peptide*** as claimed in claim 1, which is env3.

5. The ***peptide*** as claimed in claim 1, which is env4.

6. The ***peptide*** as claimed in claim 1, which is env5.

7. The ***peptide*** as claimed in claim 1, which is env6.

8. The ***peptide*** as claimed in claim 1, which is env7.

9. The ***peptide*** as claimed in claim 1, which is env8.

10. The ***peptide*** as claimed in claim 1, which is env9.

11. The ***peptide*** as claimed in claim 1, which is env10.

12. The ***peptide*** as claimed in claim 1, which is env11.

13. The ***peptide*** as claimed in claim 1, which is gag1.

L4 ANSWER 19 OF 23 USPATFULL
92:1696 Cloned DNA sequences related to the entire genomic RNA of human immunodeficiency virus II (***HIV*** -2), polypeptides encoded by these DNA sequences and use of these DNA clones and polypeptides in diagnostic kits.
Alizon, Marc , Paris, France
Montagnier, Luc, Le Pleissis Robinson, France
Geutard, Denise, Paris, France
Clavel, Francois, Rockville, MD, United States
Sonigo, Pierre, Paris, France
Guyader, Mireille, Paris, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5079342 19920107
APPLICATION: US 1987-13477 19870211 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for diagnosing an ***HIV*** -2 (***LAV*** -II) infection and a kit containing reagents for the same is disclosed. These reagents include cDNA probes which are capable of hybridizing to at least a portion of the genome of ***HIV*** -2. In one embodiment, the DNA probes are capable of hybridizing to the entire genome of ***HIV*** -2. These reagents also include polypeptides encoded by some of these DNA sequences.
CLM What is claimed is:
1. A ***peptide*** comprising immunological properties of a first portion of the ***envelope*** glycoprotein of a ***HIV*** -2 virus, wherein said ***peptide*** comprises no more than about 40 amino acid residues, said first portion of the ***envelope*** glycoprotein is antigenic or is capable of eliciting the production of antibodies directed to the ***peptide*** alone or when conjugated to a carrier molecule, and said ***envelope*** glycoprotein comprises an amino acid sequence substantially as follows: ##STR4##

2. A ***peptide*** according to claim 1, comprising an amino acid sequence of either of the following formulas: XR--A-E-YL-DQ--L--WGC----- CZ XA-E-YL-DZ, wherein X and Z are OH or NH.sub.2, or at least one of X

and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RVTAIEKYLQDQARLNSWGCAFRQVC, or AIEKYLQDQ.

3. A ***peptide*** according to claim 1, comprising an amino acid sequence of either of the following formulas: X--E--Q-QQEKN--EL--L---Z, or XQ-QQEKNZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: SKSLEQAQIQQEKNMYELQKLNSW, or QIQQEKN.

4. A ***peptide*** according to claim 1, comprising an amino acid sequence of either of the following formulas: XEL--YK-V-I-P-G-APTK-KR----Z, or XYK-V-I-P-G-APTK-KRZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: ELGDYKLVEITPIGFAPTKEKRYSSAH, or YKLVEITPIGFAPTKEK.

5. An antigenic composition comprising at least one ***peptide*** according to claims 2, 3, or 4, or at least an oligomer of the ***peptide*** that comprises the capability to specifically recognize the presence of anti- ***HIV*** -2 antibodies.

6. A ***peptide*** according to claim 1, comprising an amino acid sequence of one of the following formulas: X----VTV-YGVP-WK-AT--LFCA-Z, or XVTV-YGVP-WK-ATZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: CTQYVTVFYGVPTWKNATIPLFCAT, or VTVFYGVPTWKNAT.

7. A ***peptide*** according to claim 6, comprising an amino acid sequence of one of the following formulas: CTQYVTVFYGVPTWKNATIPLFCAT, or VTVFYGVPTWKNAT.

8. A ***peptide*** according to claim 1, comprising an amino acid sequence of one of the following formulas: X---QE--LNVTE-F--W-NZ, or XLNVTE-FZ wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and

wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of the following ***peptide*** sequence: DDYQEITLNVTEAFDAWNN.

9. A ***peptide*** according to claim 8, comprising an amino acid sequence of the following formula: DDYQEITLNVTEAFDAWNN.

10. A ***peptide*** according to claim 1, comprising an amino acid sequence of one of the following formulas: XL---S-KPCVKLTPLCV--KZ, or XKPCVKLTPLCVZ, or XS-KPCVKLTPLCVZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of the following ***peptide*** sequence: ETSIKPCVKLTPLCVAMK.

11. A ***peptide*** according to claim 10, comprising an amino acid sequence of the following formula: ETSIKPCVKLTPLCVAMK.

12. A ***peptide*** according to claim 1, comprising an amino acid sequence of one of the following formulas: X---N-S-IT--C-Z, or XN-S-ITZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of the following ***peptide*** sequence: NHCNTSVITESCD.

13. A ***peptide*** according to claim 12, comprising an amino acid sequence of the following formula: NHCNTSVITESCD.

14. A ***peptide*** according to claim 1, comprising an amino acid sequence of the following formula: XYC-P-G-A-L-CN-TZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprised from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of the following ***peptide*** sequence: YCAPPGYALLRCNDT.

15. A ***peptide*** according to claim 14, comprising an amino acid sequence of the following formula: YCAPPGLALLRCNDT.

16. A ***peptide*** according to claim 1, comprising an amino acid sequence of the following formula: X------A-C-----W--Z wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacryl residue chosen from among those which permit the conservation of the immunological properties of the following ***peptide*** sequence: NKRPRQAWCWFKGKWKD.

17. A ***peptide*** according to claim 16, comprising an amino acid sequence of the following formula: NKRPRQAWCWFKGKWKD.

18. A ***peptide*** according to claim 1, comprising an amino acid sequence of one of the following formulas: X-G-DPE------NC-GEF-YCN----- NZ, or XNC-GEF-YCNZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permits the conservation of the immunological properties of either of the following ***peptide*** sequences: KGSDPEVAYMWTNCRGEFLYCNMTWFLN, or NCRGEFLYCN,

19. A ***peptide*** according to claim 18, comprising an amino acid sequence of one of the following formulas: KGSDPEVAYMWTNCRGEFLYCNMTWFLYN , or MCRGEFLYCN.

20. A ***peptide*** according to claim 1, comprising an amino acid sequence of one of the following formulas: X-----C-IKQ-I------G---YZ, or XC-IKQ-IZ, wherein X and Z are OH or NH.sub.2, or least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RNYAPCHIKQIINTWHKVGRNVY, or or CHIKQII.

21. A ***peptide*** according to claim 20, comprising an amino acid sequence of one of the following formulas: RNYACHIKQIINTWHKVGRNVY, or or CHIKQII.

22. An immunogenic composition comprising at least one ***peptide*** according to any one of the claims 6-21, or at least one oligomer of said ***peptide*** or said ***peptide*** conjugated to a carrier molecule, and a pharmacologically acceptable vehicle, wherein said immunogenic composition is suitable for injection into a warm blooded mannal, and said ***peptide*** is capable of eliciting antibody production against the ***peptide*** in sufficient quantities to form an effective immunocomplex with the entire ***HIV*** -2 retrovirus or with its corresponding proteins.

23. An immunogenic composition according to claim 22, wherein said immunogenic composition further comprises a second portion of the ***envelope*** glycoprotein of the ***HIV*** -2 virus, wherein said second portion and a portion of an ***envelope*** glycoprotein of ***HIV*** -1 have an amino acid homology of greater than 50%.

24. The antigenic ***peptide*** gag1 comprising an amino acid sequence of the following formula: XNCKLVLKGLGMNPTLEEMLTAZ wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of the following

peptide sequence: XNCKLVLKGLGMNPTLEEMLTA.

25. An antigenic composition comprising at least one gag1 ***peptide*** according to claim 24 or at least an oligomer of this ***peptide*** that comprises the capability to be recognized by human bological fluids such as serum containing anti- ***HIV*** -2 antibodies and under appropriate conditions anti- ***HIV*** -1 antibodies.

L4 ANSWER 18 OF 23 USPATFULL
94:35490 Methods and kits for diagnosing human immunodeficiency virus type 2(***HIV*** -2).
Alizon, Marc , Paris, France
Montagnier, Luc, Le Plessis Robinson, France
Guetard, Denise, Paris, France
Clavel, Francois, Rockville, MD, United States
Sonigo, Pierre, Paris, France
Guyader, Mireille, Paris, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5306614 19940426
APPLICATION: US 1991-810824 19911220 (7)
PRIORITY: FR 1986-911 19860122
FR 1986-1635 19860206
FR 1986-1985 19860213
FR 1986-3881 19860318
FR 1986-4215 19860324
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A method for diagnosing an ***HIV*** -2 (***LAV*** -II) infection and a kit containing reagents for the same is disclosed. These reagents include cDNA probes which are capable of hybridizing to at least a portion of the genome of ***HIV*** -2. In one embodiment, the DNA probes are capable of hybridizing to the entire genome of ***HIV*** -2. These reagents also include polypeptides encoded by some of these DNA sequences.

CLM What is claimed is:
1. A method for the in vitro detection of the presence or absence of antibodies which bind to ***peptides*** of a Human Immunodeficiency Virus Type 2 (***HIV*** -2) comprising: contacting a biological sample with a ***peptide*** having immunological properties of a first portion of the ***envelope*** glycoprotein of a ***HIV*** -2 virus, wherein said immunological properties comprise the ability of said ***peptide*** to specifically recognize antibodies against ***HIV*** -2; and wherein said ***peptide*** comprises no more than about 40 amino acid residues, said first portion of the ***envelope*** glycoprotein is antigenic or is capable of eliciting the production of antibodies directed to the ***peptide*** , and said ***envelope*** glycoprotein comprises an amino acid sequence substantially as follows: ##STR4##

2. A method for the in vitro detection of the presence or absence of antibodies which bind to ***peptides*** of a Human Immunodeficiency Virus Type 2 (***HIV*** -2) comprising: contacting a biological sample with one or more ***peptides*** selected from the group consisting of: (1) a ***peptide*** comprising an amino acid sequence of either of the following formulas: XR--A-E-YL-DQ--L--WGC----CZ, or XA-E-YL-DZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RVTAIEKYLQDQARLNSWGCAFRQVC, or AIEKYLQDQ; (2) a ***peptide***

comprising an amino acid sequence of either of the following formulas: X----E--Q-QQEKN--EL--L---Z, or XQ-QQEKNZ wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: SKSLEQAQIQQEKNMYELQKLNSW, or QIQQEKN; (3) a ***peptide*** comprising an amino acid sequence of either of the following formulas: XEL--YK-V-I-P-G-APTK-KR-----Z, or XYK-V-I-P-G-APTK-KRZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: ELGDYKLVEITPIGFAPTKEKRYSSAH or YKLVEITPIGFAPTKEK; (4) the antigenic ***peptide*** gag1 comprising an amino acid sequence of the following formula: XNCKLVLKGLGMNPTLEEMLTAZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: XNCKLVLKGLGMNPTLEEMLTA; (5) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X----VTV-YGVP-WK-AT--LFCA-Z, or XVTV-YGVP-WK-ATZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: CTQYVTVFYGVPTWKNATIPLFCAT, or VTVFYGVPTWKNAT; (6) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X-G-DPE------NC-GEF-YCN----NZ, or XNC-GEF-YCNZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: KGSDPEVAYMWTNCRGEFLYCNMTWFLN, or NCRGEFLYCN; (7) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X-----C-IKQ-I------G---YZ, or XC-IKQ-IZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RNYAPCHIKQIINTWHKVGRNVY, or CHIKQII; (8) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X---QE--LNVTE-F--W-NZ, or XLNVTE-FZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of immunological properties of the following ***peptide*** sequences: DDYQEITLNVTEAFDAWNN; (9) a ***peptide*** comprising an amino acid sequence of either of the following formulas: XL---S-KPCVKLTPLCV--KZ, or XKPCVKLTPLCVZ, or XS-KPCVKLTPLCVZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptides*** sequences: ETSIKPCVKLTPLCVAMK; (10) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X---N-S-IT--C-Z, or XN-S-ITZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: NHCNTSVITESCD; (11) a ***peptide*** comprising an amino acid sequence having the following formula: XYC-P-G-A-L-CN-TZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following

peptide sequence: YCAPPGYALLRCNDT; and (12) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X------A-C-----W--Z, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: NKRPRQAWCWFKGKWKD; wherein said immunological properties comprise the ability of said ***peptide*** sequences to specifically recognize antibodies against ***HIV*** -2; and detecting ***peptide*** -antibody complex formed between said ***peptide*** and antibodies present in said biological fluid.

3. The method of claim 2, wherein at least one of X and Z comprises a terminal group having from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group.

4. The method of claim 2, comprising ***peptides*** (1), (2), (3), and (4).

5. The method of claim 2, wherein ***peptide*** -antibody complex is detected by a process selected from the group consisting of enzyme-linked immunosorbent assay (ELISA), immunofluorescence assay (IFA), radioimmunoassay (RIA), and radioimmunopreciptation assay (RIPIA).

6. The method of claim 2, wherein said ***peptide*** is conjugated to a carrier molecule.

7. A diagnostic kit for the in vitro detection of the presence or absence of antibodies in a biological sample which bind to ***peptides*** of a Human Immunodeficiency Virus Type 2 (***HIV*** -2) comprising: a ***peptide*** composition comprising a ***peptide*** having immunological properties of a first portion of the ***envelope*** glycoprotein of a ***HIV*** -2 virus, wherein said immunological properties comprise the ability of said ***peptide*** to specifically recognize antibodies against ***HIV*** -2; and wherein said ***peptide*** comprises not more than about 40 amino acid residues, said first portion of the ***envelope*** glycoprotein is antigenic or is capable of eliciting the production of antibodies directed to the ***peptide*** , and said ***envelope*** glycoprotein comprises an amino acid sequence substantially as follows: ##STR5##

8. A diagnostic kit for the in vitro detection of the presence or absence of antibodies in a biological sample which bind to ***peptides*** of a Human Immunodeficiency Virus Type 2 (***HIV*** -2) comprising: a ***peptide*** composition containing one or more ***peptides*** selected from the group consisting of: (1) a ***peptide*** comprising an amino acid sequence of either of the following formulas: XR--A-E-YL-DQ--L--WGC-----CZ, or XA-E-YL-DZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RVTAIEKYLQDQARLNSWGCAFRQVC, or AIEKYLQDQ; (2) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X----E--Q-QQEKN--EL--L---Z, or XQ-QQEKNZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the

conservation of the immunological properties of the either of following ***peptide*** sequences: SKSLEQAQIQQEKNMYELQKLNSW, or QIQQEKN; (3) a ***peptide*** comprising an amino acid sequence of either of the following formulas: XEL--YK-V-I-P-G-APTK-KR-----Z, or XYK-V-I-P-G-APTK-KRZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: ELGDYKLVEITPIGFAPTKEKRYSSAH, or YKLVEITPIGFAPTKEK; (4) the ***peptide*** gag1 comprising an amino acid sequence of the following formula: XNCKLVLKGLGMNPTLEEMLTAZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: XNCKLVLKGLGMNPTLEEMLTA; (5) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X----VTV-TGVP-WK-AT--LFCA-Z, or XVTV-YGVP-WK-ATZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: CTQYVTVFYGVPTWKNATIPLFCAT, or VTVFYGVPTWKNAT; (6) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X-G-DPE------NC-GEF-YCN----NZ, or XNC-GEF-YCNZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: KGSDPEVAYMWTNCRGEFLYCNMTWFLN, or NCNRGEFLYCN; (7) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X-----C-IKQ-I------G---YZ, or XC-IKQ-IZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RNYAPCHIKQIINTWHKVGRNVY, or CHIKQII; (8) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X---QE--LNVTE-F--W-NZ, or XLNVTE-FZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: DDYQEITLNVTEAFDAWNN; (9) a ***peptide*** comprising an amino acid sequence of either of the following formulas: XL---S-KPCVKLTPLCV--KZ, or XKPCVKLTPLCVZ, or XS-KPCVKLTPLCVZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: ETSIKPCVKLTPLCVAMK; (10) a ***peptide*** comprising an amino acid sequence of either of the following formulas: X---N-S-IT--C-Z, or XN-S-ITZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: NHCNTSVITESCD; (11) a ***peptide*** comprising an amino acid sequence having the following formulas: XYC-P-G-A-L-CN-TZ, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: YCAPPGYALLRCNDT; and (12) a ***peptide*** comprising an amino acid sequence of the following formula: X------A-C-----W--Z, wherein X and Z are OH or NH.sub.2, and wherein each of the hyphens corresponds to an aminoacyl residue selected from

the group consisting of those which permit the conservation of the immunological properties of the following ***peptide*** sequence: NKRPRQAWCWFKGKWKD; wherein said immunological properties comprise the ability of said ***peptide*** sequences to specifically recognize antibodies against ***HIV*** -2; reagents for the detection of the formation of ***peptide*** -antibody complex; and a biological reference sample lacking antibodies recognized by said ***peptide*** composition, wherein said ***peptide*** composition, reagents, and biological reference material are present in an amount sufficient to perform said detection of ***peptide*** -antibody complex formed between said ***peptide*** and antibodies present in the biological sample.

9. The kit of claim 8, wherein at least one of X and Z comprises a terminal group having from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group.

10. The kit of claim 8, comprising ***peptides*** (1), (2), (3), and (4).

11. The kit of claim 8, wherein said ***peptide*** is conjugated to a carrier molecule.

L4 ANSWER 14 OF 23 USPATFULL
1998:48164 Diagnostic kits and methods for detecting antibodies to ***LAV*** viruses.
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Sonigo, Pierre, Paris, France
Wain-Hobson, Simon, Montigny les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5747242 19980505
APPLICATION: US 1995-466907 19950606 (8)
PRIORITY: EP 1986-401380 19860623
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A variant of a ***LAV*** virus, designated ***LAV*** .sub.ELI and cable of causing ***AIDS*** . The cDNA and antigens of the ***LAV*** .sub.ELI virus can be used for the diagnosis of ***AIDS*** an pre- ***AIDS*** .
CLM What is claimed is:
1. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic ***peptide*** , and then detecting the immunological reaction between said ***peptide*** and said antibody, wherein said isolated or synthetic ***peptide*** comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR1## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, and amino-acyl residues 531-877 of an

envelope glycoprotein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.BRU as set forth in FIG. 3.

2. The method of claim 1, wherein said amino acid sequence is selected from the group consisting of amino-acyl residues 37 to 130, 211 to 289, and 488 to 530.

3. The method of claim 1, wherein said amino acid sequence comprises amino-acyl residues 490 to 620 or 680 to 700.

4. The method of claim 1, wherein said amino acid sequence is selected from the group consisting of: amino-acyl residues 1 to 530; amino-acyl residues 34 to 530; and amino-acyl residues 531 to 877.

5. The method of claim 1, wherein said lymphadenopathy associated virus is ***LAV*** .sub.ELI.

6. The method of claim 1, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said ***peptide*** into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody- ***peptide*** complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

7. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic ***peptide*** , and then detecting the immunological reaction between said ***peptide*** and said antibody, wherein said isolated or synthetic ***peptide*** comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR2## wherein, said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p25 ***peptide*** comprising amino-acyl residues 138-385 of gag protein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.BRU as set forth in FIG. 3.

8. The method of claim 7, wherein said lymphadenopathy associated virus is ***LAV*** .sub.ELI.

9. The method of claim 7, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said ***peptide*** into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody- ***peptide*** complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

10. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic ***peptide*** , and then detecting the immunological reaction between said ***peptide*** and said antibody, wherein said isolated or

synthetic ***peptide*** comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR3## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L, is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p13 ***peptide*** comprising amino-acyl residues 385-519 of gag protein of ***LAV*** .sub.ELL virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.RM as set forth in FIG. 3.

11. The method of claim 10, wherein said lymphadenopathy associated virus is ***LAV*** .sub.ELI.

12. The method of claim 10, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said ***peptide*** into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody- ***peptide*** complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

13. A method for the in vitro detection of an antibody directed against a lymphadenopathy associated virus in a human body fluid, comprising the steps of contacting said body fluid with an isolated or synthetic ***peptide*** , and then detecting the immunological reaction between said ***peptide*** and said antibody, wherein said isolated or synthetic ***peptide*** comprises an amino acid sequence that is a fragment of the following amino acid sequence: ##STR4## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment is selected from the group consisting of amino-acyl residues 14-20, amino-acyl residues 50-59, amino-acyl residues 371-383, amino-acyl residues 410-430, and amino-acyl residues 536-557 of the pol protein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.RM as set forth in FIG. 3.

14. The method of claim 13, wherein said lymphadenopathy associated virus is ***LAV*** .sub.ELI.

15. The method of claim 13, wherein said contacting and detecting steps comprise: a) depositing a predetermined amount of said ***peptide*** into wells of a microplate; b) introducing increasing dilutions of said body fluid into said wells; c) incubating said microplate to allow the formation of antibody- ***peptide*** complexes; d) washing the microplate; e) adding to said wells a labeled antibody directed against immunoglobulins; and then f) determining whether an antigen-antibody complex has formed in said wells.

16. A diagnostic kit for the in vitro detection of antibodies against a ***LAV*** virus, which kit comprises an antigen selected from the group consisting of the following: an isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR5## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, F is glutamic

acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises at least one amino acid sequence selected from the group consisting of amino-acyl residues 37-130, amino-acyl residues 211-289, amino-acyl residues 488-530, amino-acyl residues 490-620, amino-acyl residues 680-700, amino-acyl residues 1-530, amino-acyl residues 34-530, and amino-acyl residues 531-877 of an ***envelope*** glycoprotein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.BRU as set forth in FIG. 3; an isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following, amino acid sequence: ##STR6## wherein, said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p25 ***peptide*** comprising amino-acyl residues 138-385 of gag protein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.BRU as set forth in FIG. 3; an isolated or synthetic ***peptide*** comprising an amino acid sequence that is a fragment of the following amino acid sequence: ##STR7## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment comprises a p13 ***peptide*** comprising amino-acyl residues 385-519 of gag protein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.BRU as set forth in FIG. 3; and an isolated or synthetic ***peptide*** comprising an amino acid sequence having a fragment of the following amino acid sequence: ##STR8## wherein, in said amino acid sequence, A is alanine, C is cysteine, D is aspartic acid, E is glutamic acid, F is phenylalanine, G is glycine, H is histidine, I is isoleucine, K is lysine, L is leucine, M is methionine, N is asparagine, P is proline, Q is glutamine, R is arginine, S is serine, T is threonine, V is valine, W is tryptophan, and Y is tyrosine, wherein said fragment is selected from the group consisting of amino-acyl residues 14-20, amino-acyl residues 50-59, amino-acyl residues 371-383, amino-acyl residues 410-430, and amino-acyl residues 536-557 of the pol protein of ***LAV*** .sub.ELI virus, and wherein the hyphens represent a gap introduced to align the sequence with ***LAV*** .sub.BRU as set forth in FIG. 3; a reagent or reagents for detecting a ***peptide*** -antibody complex; a biological reference material lacking antibodies that bind to said ***peptide*** or ***peptides*** ; and a comparison sample comprising antibodies that bind to said ***peptide*** or ***peptides*** .

L4 ANSWER 12 OF 23 USPATFULL
1998:75745 DNA fragments obtained from a novel human immunodeficiency virus designated ***LAV*** .sub.MAL.
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US 5773602 19980630
APPLICATION: US 1993-154397 19931118 (8)
PRIORITY: FR 1986-401380 19860623
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel human immunodeficiency virus type 1 (***HIV*** -1) isolate, designated lymphadenopathy-associated virus strain MAL, or ***LAV*** .sub.MAL, was molecularly cloned and characterized. Nucleotide sequence analysis demonstrated that the viral genome of ***LAV*** .sub.MAL is 9229 nucleotides long. This retrovirus contains the canonical gag, pol, and ***env*** genes, as well as ancillary genes encoding Vif (or Q), Vpr (or R), Tat (or S), and Nef (or F). This virus differs significantly, at both the nucleotide and amino acid sequence levels, from prototypical ***HIV*** isolates (e.g., ***HTLV*** -III, ***LAV*** .sub.BRU, and ***ARV***). DNA fragments corresponding to the various gene products and regulatory regions are disclosed. These fragments are useful, inter alia, as probes in diagnostic assays and for the generation of recombinant proteins.

CLM What is claimed is:

1. A DNA fragment having a nucleotide sequence selected from the group consisting of: a sequence having nucleotides 1 to 96, which is the long terminal repeat R region of ***LAV*** .sub.MAL ; a sequence having nucleotides 97 to 179, which is the 5' long terminal repeat U5 region of ***LAV*** .sub.MAL ; a sequence having nucleotides 8676 to 9133, which is the 3' long terminal repeat U3 region of ***LAV*** .sub.MAL ; a sequence having nucleotides 9134 to 9229, which is the 3' long terminal repeat U3 region of ***LAV*** .sub.MAL ; a sequence having nucleotides 5405 to 5620, which is the tat coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 5134 to 5421, which is the vpr coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 8380 to 9006, which is the nef coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 350 to 1864, which is the gag coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 1663 to 4668, which is the pol coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 5799 to 8375, which is the ***env*** coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 764 to 1501, which is the gag p25 coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 1502 to 1864, which is the gag p13 coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 5799 to 5885, which corresponds to amino acids 1-33 of the ***env*** coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 5886 to 7337, which corresponds to amino acids 34 to 530 of the gp110 ***env*** coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 5895 to 6176, which corresponds to amino acids 37 to 130 of the ***env*** coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 6399 to 6635, which corresponds to amino acids 211 to 289 of the ***env*** coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 7212 to 7337, which corresponds to amino acids 488 to 530 of the ***env*** coding region of ***LAV*** .sub.MAL ; a sequence having nucleotides 7215 to 7604, which corresponds to amino acids 490 to 620 of the ***env*** coding region of ***LAV*** .sub.MAL ; and a sequence having nucleotides 7782 to 7844, which corresponds to amino acids 680 to 700 of the ***env*** coding region of ***LAV*** .sub.MAL.

2. The DNA fragment as claimed in claim 1, wherein said fragment is operatively linked to a promoter sequence.

3. A DNA fragment as claimed in claim 1, wherein said fragment has a nucleotide sequence having nucleotides 1 to 96, which is the long terminal repeat R region of ***LAV*** .sub.MAL.

4. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 97 to 179, which is the 5' long terminal repeat U5 region of ***LAV*** .sub.MAL.

5. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 8676 to 9133, which is the 3' long terminal repeat U3 region of ***LAV*** .sub.MAL.

6. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 9134 to 9229, which is the 3' long terminal repeat U3 region of ***LAV*** .sub.MAL.

7. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5405 to 5620, which is the tat coding region of ***LAV*** .sub.MAL.

8. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5134 to 5421, which is the vpr coding region of ***LAV*** .sub.MAL.

9. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 8380 to 9006, which is the nef coding region of ***LAV*** .sub.MAL.

10. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 350 to 1864, which is the gag coding region of ***LAV*** .sub.MAL.

11. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 1663 to 4668, which is the pol coding region of ***LAV*** .sub.MAL.

12. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5799 to 8375, which is the ***env*** coding region of ***LAV*** .sub.MAL.

13. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 764 to 1501, which is the gag p25 coding region of ***LAV*** .sub.MAL.

14. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 1502 to 1864, which is the gag p13 coding region of ***LAV*** .sub.MAL.

15. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5799 to 5885, which corresponds to amino acids 1-33 of the ***env*** coding region of ***LAV*** .sub.MAL.

16. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5886 to 7337, which corresponds to amino acids 34 to 530 of the gp110 ***env*** coding region of ***LAV*** .sub.MAL.

17. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 5895 to 6176, which corresponds to amino acids 37 to 130 of the ***env*** coding region of ***LAV*** .sub.MAL.

18. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 6399 to 6635, which corresponds to amino

acids 211 to 289 of the ***env*** coding region of ***LAV*** .sub.MAL.

19. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 7212 to 7337, which corresponds to amino acids 488 to 530 of the ***env*** coding region of ***LAV*** .sub.MAL.

20. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 7215 to 7604, which corresponds to amino acids 490 to 620 of the ***env*** coding region of ***LAV*** .sub.MAL.

21. A DNA fragment as claimed in claim 1, wherein said fragment has a sequence having nucleotides 7782 to 7844, which corresponds to amino acids 680 to 700 of the ***env*** coding region of ***LAV*** .sub.MAL.

22. A recombinant vector comprising a DNA fragment of any one of claims 1-21.

L4 ANSWER 11 OF 23 USPATFULL
1998:128076 Purification, cloning, and characterization of a novel human immunodeficiency virus ***LAV*** .sub.MAL.
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Wain-Hobson, Simon, Montigney Les Bretonneux, France
Montagnier, Luc, Le Plessis Robinson, France
Institut Pasteur, Paris, France (non-U.S. corporation)
US 5824482 19981020
APPLICATION: US 1995-471474 19950606 (8)
PRIORITY: FR 1986-40138 19860623
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB An ***HIV*** isolate, ***LAV*** .sub.MAL, has been purified, sequenced, and characterized at the genetic level. The entire nucleic acid sequence of the viral genome, the encoded amino acid sequences, and the open reading frames found in the genome are disclosed. Specific ***peptides*** relating to the ***envelope*** glycoprotein of the viral genome are discussed. These ***peptides*** can be used in diagnostic methods and kits for detecting the presence of an ***HIV*** virus.
CLM What is claimed is:
1. A purified virus, designated ***LAV*** .sub.MAL, having CNCM biological deposit number I-641.

2. A method for the in vitro detection of the presence of an antibody directed against a ***LAV*** virus in a human body fluid, which comprises contacting said body fluid with an antigen obtained from a virus ***LAV*** .sub.MAL, said antigen selected from the group consisting of: a purified or synthetic ***peptide*** having an amino acid sequence of one of the open reading frames set forth in FIGS. 7A-7I; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 37-130 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 211-289 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 488-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues

490-620 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 680-700 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 1-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 34-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; and a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 531-877 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL and detecting the immunological reaction between said antigen and said antibody.

3. The method of claim 2 comprising: (a) depositing a predetermined amount of said antigen into a cup of a titration microplate; (b) introducing increasing dilutions of said body fluid into said cup; (c) incubating said microplate; (d) washing the microplate with a buffer; (e) adding into said cup a labeled antibody directed against blood immunoglobulins; and then (f) determining whether an antigen-antibody-complex has formed in said cup which is indicative of the presence of a ***LAV*** antibody in said body fluid.

4. A diagnostic kit for the in vitro detection of antibodies against a ***LAV*** virus comprising (a) an antigen selected from the group consisting of: a purified or synthetic ***peptide*** (having the amino acid sequence of one of the open reading frames set forth in FIGS. 7A-7F; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 37-130 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 211-289 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 488-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 490-620 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 680-700 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 1-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL ; a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 34-530 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL and a purified or synthetic ***peptide*** having the amino acid sequence set forth as residues 531-877 of the ***envelope*** glycoprotein of ***LAV*** .sub.MAL, (b) reagents for the detection of the formation of antigen-antibody complex, and (c) a biological reference sample lacking antibodies recognized by said antigen, wherein the ***peptide*** , reagents, and biological reference sample are present in an amount sufficient to perform the detection of antigen-antibody complex formed between said ***peptide*** and antibodies present in said biological reference sample.

L4 ANSWER 8 OF 23 USPATFULL
1999:4320 Nucleotide sequences of human immunodeficiency virus type 2 (***HIV*** -2), probes of ***HIV*** -2, and methods of using these probes.
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for diagnosing an ***HIV*** -2 (***LAV*** -II) infection and a kit containing reagents for the same is disclosed. These reagents include cDNA probes which are capable of hybridizing to at least a portion of the genome of ***HIV*** -2. In one embodiment, the DNA probes are capable of hybridizing to the entire genome of ***HIV*** -2. These reagents also include polypeptides encoded by some of these DNA sequences.
CLM What is claimed is:

1. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of either of the following formulas: XR--A-E-D-YL-DQ--L--WGC-----CZ or XA-E-D-YL-DZ, wherein X and Z are OH or NH.sub.2 or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens corresponds to an aminoacyl residue chosen from among those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: RVTAIEKYLQDQARLNSWGCAFRQVC or AIEKYLQDQ.

2. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of either of the following formulas: X--E--Q-QQEKN--EL--L---Z or XQ-QQEKNZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: SLEQAQIQQEKNMYELQKLNSW or QIQQEKN.

3. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of either of the following formulas: XEL--YK-V-I-P-G-APTK-KR-----Z or XYK-V-I-P-G-APTK-KRZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: ELGDYKLVEITPIGFAPTKEKRYSSAH or YKLVEITPIGFAPTKEK.

4. A purified nucleic acid encoding a ***peptide*** comprising an

amino acid sequence of either of the following formulas: X----VTV-YGVP-WK-AT--LPCA-Z or XVTV-YGVP-WK-ATZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: CTQYVTVFYGVPTWKNATIPLFCAT, VTVFYGVPTWKNAT, EKLWVTVYYGVPVWKEATTTLFCAS, or VTVYYGVPVWKEAT.

5. The nucleic acid of claim 4, wherein the the amino acid sequence has one of the following formulas: CTQYVTVFYGVPTWKNATIPLFCAT, VTVFYGVPTWKNAT, EKLWVTVYYGVPVWKEATTTLFCAS, VTVYYGVPVWKEAT, EDLWVTVYYGVPVWKEATTTLFCAS, or DNLWVTVYYGVPVWKEATTTLFCAS.

6. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of either of the following formulas: X---QE--L-NVTE-F--W-NZ or XL-NVTE-FZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: DDYQEITL-NVTEAFDAWNN, L-NVTE, PNPQEVVLVNVTENFNMWKN, or LVNVTE.

7. The nucleic acid of claim 6, wherein the nucleic acid encodes an amino acid sequence of one of the following formulas: DDYQEITL-NVTEAFDAWNN, L-NVTEAF, PNPQEVVLVNVTENFNMWKN, LVNVTENF, PNPQEIELENVTEGFNMWKN, LENVTEGF, PNPQEIALENVTENFNMWKN, or LENVTENF. 8.

8. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of one of the following formulas: XL---S-KPCVKLTPLCV--KZ, XKPCVKLTPLCVZ, or XS-KPCVKLTPLCVZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: ETSIKPCVKLTPLCVAMK, DQSLKPCVKLTPLCVSLK, KPCVKLTPLCV, or SLKPCVKLTPLCV.

9. The nucleic acid of claim 8, wherein the nucleic acid encodes an amino acid sequence having one of the following formulas: ETSIKPCVKLTPLCVAMK, DQSLKPCVKLTPLCVSLK, DQSLKPCVKLTPLCVTLN, or PCVKLTPLC.

10. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of one of the following formulas: X---N-S-IT--C-Z or XN-S-ITZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen

from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: NHCNTSVITESCD, NTSVIT, TSCNTSVITQACP, or NTSAIT.

11. The nucleic acid of claim 10, wherein the nucleic acid encodes a ***peptide*** comprising an amino acid sequence of one of the following formulas: NHCNTSVITESCD, NTSVIT, TSCNTSVITQACP, INCNTSVITQACP, INCNTSAITQACP, or NTSAIT.

12. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of the following formula: XYC-P-G-A-L-C-N-TZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of either of the following ***peptide*** sequences: YCAPPGYALLRC-NDT or YCAPAGFAILKCNNKT.

13. The nucleic acid of claim 12, wherein the nucleic acid encodes a ***peptide*** comprising an amino acid sequence of one of the following formulas: YCAPPGYALLRC-NDT, YCAPAGFAILKCNNKT, YCAPAGFAILKCNDKK, or YCAPAGFAILKCRDKK.

14. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of the following formula: X----A-C------W--Z, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: NKRPRQAWCWFKG-KWKD or N--MRQAHCNISRAKWNA.

15. The nucleic acid of claim 14, wherein the nucleic acid encodes a ***peptide*** comprising an amino acid sequence of one of the following formulas: NKRPRQAWCWFKG-KWKT, N--MRQAHCNISRAKWNA, D--IRRAYCTINETEWDK, or I--IGQAHCNISRAQWSK. 16.

16. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of one of the following formulas: X-G-DPE------NC-GEF-YCN-----NZ or XNC-GEF-YCNZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: KGSDPEVAYMWTNCRGEFLYCNMTWFLN, NCRGEFLYCN, -GGDPEIVTHSFNCGGEFFYCNSTQLFN, or NCGGEFFYCN.

17. The nucleic acid of claim 16, wherein the nucleic acid encodes a ***peptide*** of one of the following formulas: KGSDPEVAYMWTNCRGEFLYCNMTWFLN, NCRGEFLYCN, -GGDPEIVTHSFNCGGEFFYCNSTQLFN, NCGGEFFYCN, -GGDPEITTHSFNCRGEFFYCNTSKLFN, NCRGEFFYCN, or -GGDPEITTHSFNCGGEFFYCNTSGLFN.

18. A purified nucleic acid encoding a ***peptide*** comprising an amino acid sequence of one of the following formulas: X-----C-IKQ-I------G---YZ or XC-IKQ-IZ, wherein X and Z are OH or NH.sub.2, or at least one of X and Z comprises a terminal group comprising from one to five amino acid residues, provided that the immunological properties of the ***peptide*** having the terminal group shall not be essentially modified from the ***peptide*** lacking the terminal group, and wherein each of the hyphens correspond to an aminoacyl residue chosen from those which permit the conservation of the immunological properties of one of the following ***peptide*** sequences: RNYAPCHIKQIINTWHKVGRNVY, CHIKQII, TITLPCRIKQFINMWQEVGKAMY, or CRIKQFI.

19. The nucleic acid of claim 18, wherein the nucleic acid encodes a ***peptide*** comprising an amino acid sequence of one of the following formulas: RNYAPCHIKQIINTWHKVGRNVY, CHIKQII, TITLPCRIKQFINMWQEVGKAMY, CRIKQFI, SITLPCRIKQIINMWQKTCKAMY, CRIKQII, or NITLQCRIKQIIKMVAGR-KAIY.

20. A purified nucleic acid encoding a ***peptide*** , gag1, having the following formula: XNCKLVLKGLGMNPTLEEMLTAZ, in which X and Z are OH or NH.sub.2 or, to the extent that the immunological properties of the natural ***peptides*** lacking these groups shall not be essentially modified, the groups having from one to five amino acid residues, and each of the hyphens corresponding to an aminoacyl residue chosen from those which permit the conservation for the ***peptide*** characterized above of the immunological properties of the following ***peptide*** sequence: XNCKLVLKGLGMNPTLEEMLTAZ.

21. A method for detecting the presence or absence of Human Immunodeficiency Virus Type 2 (***HIV*** -2) comprising: (1) contacting a sample suspected of containing viral genetic material of ***HIV*** -2 with at least one nucleotide probe, and (2) detecting hybridization between the nucleotide probe and the viral genetic material in the sample, wherein said nucleotide probe is complementary to the full-length sequence of the purified nucleic acid selected from the group consisting of the purified nucleic acids of claims 84-103.

L4 ANSWER 4 OF 23 USPATFULL
1999:141307 Amino acid DNA sequences related to genomic RNA of human immunodeficiency virus (***HIV*** -1).
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US 5980900 19991109
APPLICATION: US 1991-751059 19910828 (7)
PRIORITY: FR 1984-16013 19841018
GB 1984-29099 19841116
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention is in the field of lymphadenopathy virus which has been desogmated Human Immunodeficiency Virus Type 1 (***HIV*** -1) This invention relates to a diagnostic means and method to detect the presence of DNA, RNA or antibodies of the lymphadenopathy retrovirus associated with the acquired immune deficiency syndrome or of the lymphadenopathy syndrome by the use of DNA fragments or the

peptides encoded by said DNA fragments. The invention further relates to the DNA fragments, vectors comprising them and the proteins expressed.

CLM What is claimed is:

1. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acid 8 to 23 of the ***env*** gene, where in the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Met-Arg-Val-Lys-Glu-Lys-Tyr-Gln-His-Leu-Trp-Arg-Trp-Gly-Trp-Lys-.

2. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 63 to 78 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Ser-Asp-Ala-Lys-Ala-Tyr-Asp-Thr-Glu-Val-His-Asn-Val-Trp-Ala-Thr-.

3. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 82 to 90 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Val-Pro-Thr-Asp-Pro-Asn-Pro-Gln-Glu-.

4. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 97 to 123 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Thr-Glu-Asn-Phe-Asn-Met-Trp-Lys-Asn-Asp-Met-Val-Glu-Gln-Met-His-Glu-Asp-Ile-Ile-Ser-Leu-Trp-Asp-Gln-Ser-Leu-.

5. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 127 to 183 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Val-Lys-Leu-Thr-Pro-Leu-Cys-Val-Ser-Leu-Lys-Cys-Thr-Asp-Leu-Gly-Asn-Ala-Thr-Asn-Thr-Asn-Ser-Ser-Asn-Thr-Asn-Ser-Ser-Ser-Gly-Glu-Met-Met-Met-Glu-Lys-Gly-Glu-Ile-Lys-Asn-Cys-Ser-Phe-Asn-Ile-Ser-Thr-Ser-Ile-Arg-Gly-Lys-Val-Gln-Lys-.

6. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 197 to 201 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Asp-Ile-Ile-Pro-Ile-Asp-Asn-Asp-Thr-Thr-.

7. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 239 to 294 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Lys-Cys-Asn-Asn-Lys-Thr-Phe-Asn-Gly-Thr-Gly-Pro-Cys-Thr-Asn-Val-Ser-Thr-Val-Gln-Cys-Thr-His-Gly-Ile-Arg-Pro-Val-Val-Ser-Thr-Gln-Leu-Leu-Leu-Asn-Gly-Ser-Leu-Ala-Glu-Glu-Glu-Val-Val-Ile-Arg-Ser-Ala-Asn-Phe-Thr-Asp-Asn-Ala-Lys-.

8. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 300 to 327 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Asn-Gln-Ser-Val-Glu-Ile-Asn-Cys-Thr-Arg-Pro-Asn-Asn-Asn-Thr-Arg-Lys-Ser-Ile-Arg-Ile-Gln-Arg-Gly-Pro-Gly-Arg-.

9. An amino acid sequence of Human Immunodeficiency Virus Type 1 (

HIV -1), consisting essentially of amino acids 334 to 381 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Lys-Ile-Gly-Asn-Met-Arg-Gln-Ala-His-Cys-Asn-Ile-Ser-Arg-Ala-Lys-Trp-Asn-Ala-Thr-Leu-Lys-Gln-Ile-Ala-Ser-Lys-Leu-Arg-Glu-Gln-Phe-Gly-Asn-Asn-Lys-Thr-Ile-Ile-Phe-Lys-Gln-Ser-Ser-Gly-Gly-Asp-Pro-.

10. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 397 to 424 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Cys-Asn-Ser-Thr-Gln-Leu-Phe-Asn-Ser-Thr-Trp-Phe-Asn-Ser-Thr-Trp-Ser-Thr-Glu-Gly-Ser-Asn-Asn-Thr-Glu-Gly-Ser-Asp-.

11. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 466 to 500 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Thr-Arg-Asp-Gly-Gly-Asn-Asn-Asn-Asn-Gly-Ser-Glu-Ile-Phe-Arg-Pro-Gly-Gly-Gly-Asp-Met-Arg-Asp-Asn-Trp-Arg-Ser-Glu-Leu-Tyr-Lys-Tyr-Lys-Val-.

12. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 510 to 523 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Pro-Thr-Lys-Ala-Lys-Arg-Arg-Val-Val-Gln-Arg-Glu-Lys-Arg-.

13. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 551 to 577 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Val-Gln-Ala-Arg-Gln-Leu-Leu-Ser-Gly-Ile-Val-Gln-Gln-Gln-Asn-Asn-Leu-Leu-Arg-Ala-Ile-Glu-Ala-Gln-Gln-His-Leu-.

14. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 594 to 603 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Ala-Val-Glu-Arg-Tyr-Leu-Lys-Asp-Gln-Gln-.

15. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 621 to 630 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Pro-Trp-Asn-Ala-Ser-Trp-Ser-Asn-Lys-Ser-.

16. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 657 to 679 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Leu-Ile-Glu-Glu-Ser-Gln-Asn-Gln-Gln-Glu-Lys-Asn-Glu-Gln-Glu-Leu-Leu-Glu-Leu-Asp-Lys-Trp-Ala-.

17. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 719 to 758 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Arg-Val-Arg-Gln-Gly-Tyr-Ser-Pro-Leu-Ser-Phe-Gln-Thr-His-Leu-Pro-Thr-Pro-Arg-Gly-Pro-Asp-Arg-Pro-Glu-Gly-Ile-Glu-Glu-Glu-Gly-Gly-Glu-Arg-Asp-Arg-Asp-Arg-Ser-Ile-.

18. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), consisting essentially of amino acids 780 to 803 of the ***env*** gene, wherein the amino acid sequence is free of particles of said virus and the amino acid sequence comprises the following: Tyr-His-Arg-Leu-Arg-Asp-Leu-Leu-Leu-Ile-Val-Thr-Arg-Ile-Val-Glu-Leu-Leu-Gly-Arg-Arg-Gly-Trp-Glu-.

19. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6096 to about 6200; and the amino acid sequence consists essentially of the following: Asn-Ala-Thr-Asn-Thr-Asn-Ser-Ser-Asn-Thr-Asn-Ser-Ser-Ser-Gly-Glu-Met-Met-Met-Glu-Lys-Gly-Glu-Ile-Lys-Asn-Cys-Ser-Phe-Asn-Ile-Ser-Thr-Ser-Ile.

20. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6261 to about 6311; and the amino acid sequence consists essentially of the following: Asn-Asp-Thr-Thr-Ser-Tyr-Thr-Leu-Thr-Ser-Cys-Asn-Thr-Ser-Val-Ile-Thr.

21. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6390 to about 6440; and the amino acid sequence consists essentially of the following: Asn-Asn-Lys-Thr-Phe-Asn-Gly-Thr-Gly-Pro-Cys-Thr-Asn-Val-Ser-Thr-Val.

22. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6486 to about 6620; and the amino acid sequence consists essentially of the following: Leu-Asn-Gly-Ser-Leu-Ala-Glu-Glu-Glu-Val-Val-Ile-Arg-Ser-Ala-Asn-Phe-Thr-Asp-Asn-Ala-Lys-Thr-Ile-Ile-Val-Gln-Leu-Asn-Gln-Ser-Val-Glu-Ile-Asn-Cys-Thr-Arg-Pro-Asn-Asn-Asn-Thr-Arg-Lys.

23. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 6861 to about 6929; and the amino acid sequence consists essentially of the following: Asn-Ser-Thr-Gln-Leu-Phe-Asn-Ser-Thr-Trp-Phe-Asn-Ser-Thr-Trp-Ser-Thr-Glu-Gly-Ser-Asn-Leu-Thr.

24. An amino acid sequence of Human Immunodeficiency Virus Type 1 (***HIV*** -1), wherein the amino acid sequence is free of particles of said virus; the amino acid sequence is encoded by a nucleotide sequence, which extends from about nucleotide 7536 to about 7631; and the amino acid sequence consists essentially of the following: Asn-Ala-Ser-Trp-Ser-Asn-Lys-Ser-Leu-Glu-Gln-Ile-Trp-Asn-Asn-Met-Thr-Trp-Met-Glu-Trp-Asp-Arg-Glu-Ile-Asn-Asn-Tyr-Thr-Ser-Leu-Ile.

25. An immunogenic composition comprising one or more ***peptides*** according to any one of claims 1 to 24.

26. A composition consisting essentially of at least one of the amino acid sequences of Human Immunodeficiency Virus Type 1 (***HIV*** -1) selected from the group consisting of: (1) the amino acid sequence encoded by the nucleotide sequence of the ***env*** gene of

HIV -1 extending from about nucleotide 6095 to about nucleotide 6200; (2) the amino acid sequence encoded by the nucleotide sequence of the ***env*** gene of ***HIV*** -1 extending from about nucleotide 6260 to about nucleotide 6310; (3) the amino acid sequence encoded by the nucleotide sequence of the ***env*** gene of ***HIV*** -1 extending from about nucleotide 6390 to about nucleotide 6440; (4) the amino acid sequence encoded by the nucleotide sequence of the ***env*** gene of ***HIV*** -1 extending from about nucleotide 6485 to about nucleotide 6620; (5) the amino acid sequence encoded by the nucleotide sequence of the ***env*** gene of ***HIV*** -1 extending from about nucleotide 6860 to about nucleotide 6930; and (6) the amino acid sequence encoded by the nucleotide sequence of the ***env*** gene of ***HIV*** -1 extending from about nucleotide 7535 to about nucleotide 7630; wherein the amino acid sequences are free of particles of said virus.

27. An immunogenic composition comprising a ***peptide*** composition according to claim 26.

28. A composition consisting essentially of a mixture of two amino acid sequences of Human Immunodeficiency Virus Type 1 (***HIV*** -1) selected from the group consisting of: (1) amino acids 8 to 23 of the ***env*** gene having the sequence Met-Arg-Val-Lys-Glu-Lys-Tyr-Gln-His-Leu-Trp-Arg-Trp-Gly-Trp-Lys-; (2) amino acids 63 to 78 of the ***env*** gene having the sequence Ser-Asp-Ala-Lys-Ala-Tyr-Asp-Thr-Glu-Val-His-Asn-Val-Trp-Ala-Thr-; (3) amino acids 82 to 90 of the ***env*** gene having the sequence Val-Pro-Thr-Asp-Pro-Asn-Pro-Gln-Glu-; (4) amino acids 97 to 123 of the ***env*** gene having the sequence Thr-Glu-Asn-Phe-Asn-Met-Trp-Lys-Asn-Asp-Met-Val-Glu-Gln-Met-His-Glu-Asp-Ile-Ile-Ser-Leu-Trp-Asp-Gln-Ser-Leu; (5) amino acids 127 to 183 of the ***env*** gene having the sequence Val-Lys-Leu-Thr-Pro-Leu-Cys-Val-Ser-Leu-Lys-Cys-Thr-Asp-Leu-Gly-Asn-Ala-Thr-Asn-Thr-Asn-Ser-Ser-Asn-Thr-Asn-Ser-Ser-Ser-Gly-Glu-Met-Met-Met-Glu-Lys-Gly-Glu-Ile-Lys-Asn-Cys-Ser-Phe-Asn-Ile-Ser-Thr-Ser-Ile-Arg-Gly-Lys-Val-Gln-Lys-; (6) amino acids 197 to 201 of the ***env*** gene having the sequence Leu-Asp-Ile-Ile-Pro-Ile-Asp-Asn-Asp-Thr-Thr-; (7) amino acids 239 to 294 of the ***env*** gene having the sequence Lys-Cys-Asn-Asn-Lys-Thr-Phe-Asn-Gly-Thr-Gly-Pro-Cys-Thr-Asn-Val-Ser-Thr-Val-Gly-Cys-Thr-His-Gly-Ile-Arg-Pro-Val-Val-Ser-Thr-Gln-Leu-Leu-Leu-Asn-Gly-Ser-Leu-Ala-Glu-Glu-Glu-Val-Val-Ile-Arg-Ser-Ala-Asn-Phe-Thr-Asp-Asn-Ala-Lys-; (8) amino acids 300 to 327 of the ***env*** gene having the sequence Leu-Asn-Gln-Ser-Val-Glu-Ile-Asn-Cys-Thr-Arg-Pro-Asn-Asn-Asn-Thr-Arg-Lys-Ser-Ile-Arg-Ile-Gln-Arg-Gly-Pro-Gly-Arg-; (9) amino acids 334 to 381 of the ***env*** gene having the sequence Lys-Ile-Gly-Asn-Met-Arg-Gln-Ala-His-Cys-Asn-Ile-Ser-Arg-Ala-Lys-Trp-Asn-Ala-Thr-Leu-Lys-Gln-Ile-Ala-Ser-Lys-Leu-Arg-Glu-Gln-Phe-Gly-Asn-Asn-Lys-Thr-Ile-Ile-Phe-Lys-Gln-Ser-Ser-Gly-Gly-Asp-Pro-; (10) amino acids 397 to 424 of the ***env*** gene having the sequence Cys-Asn-Ser-Thr-Gln-Leu-Phe-Asn-Ser-Thr-Trp-Phe-Asn-Ser-Thr-Trp-Ser-Thr-Glu-Gly-Ser-Asn-Asn-Thr-Glu-Gly-Ser-Asp-; (11) amino acids 466 to 500 of the ***env*** gene having the sequence Leu-Thr-Arg-Asp-Gly-Gly-Asn-Asn-Asn-Asn-Gly-Ser-Glu-Ile-Phe-Arg-Pro-Gly-Gly-Gly-Asp-Met-Arg-Asp-Asn-Trp-Arg-Ser-Glu-Leu-Tyr-Lys-Tyr-Lys-Val-; (12) amino acids 510 to 523 of the ***env*** gene having the sequence Pro-Thr-Lys-Ala-Lys-Arg-Arg-Val-Val-Gln-Arg-Glu-Lys-Arg-; (13) amino acids 551 to 577 of the ***env*** gene having the sequence Val-Gln-Ala-Arg-Gln-Leu-Leu-Ser-Gly-Ile-Val-Gln-Gln-Gln-Asn-Asn-Leu-Leu-Arg-Ala-Ile-Glu-Ala-Gln-Gln-His-Leu-; (14) amino acids 594 to 603 of the ***env*** gene having the sequence Ala-Val-Glu-Arg-Tyr-Leu-Lys-Asp-Gln-Gln-; (15) amino acids 621 to 630 of the ***env*** gene having the sequence Pro-Trp-Asn-Ala-Ser-Trp-Ser-Asn-Lys-Ser-; (16) amino acids 657 to 679 of the ***env*** gene having the sequence

Leu-Ile-Glu-Glu-Ser-Gln-Asn-Gln-Gln-Glu-Lys-Asn-Glu-Gln-Glu-Leu-Leu-Glu-Leu-Asp-Lys-Trp-Ala-; (17) amino acids 719 to 758 of the ***env*** gene having the sequence Arg-Val-Arg-Gln-Gly-Tyr-Ser-Pro-Leu-Ser-Phe-Gln-Thr-His-Leu-Pro-Thr-Pro-Arg-Gly-Pro-Asp-Arg-Pro-Glu-Gly-Ile-Glu-Glu-Glu-Gly-Gly-Glu-Arg-Asp-Arg-Asp-Arg-Ser-Ile-; and (18) amino acid 780 to 803 of the ***env*** gene having the sequence Tyr-His-Arg-Leu-Arg-Asp-Leu-Leu-Leu-Ile-Val-Thr-Arg-Ile-Val-Glu-Leu-Leu-Gly-Arg-Arg-Gly-Trp-Glu-; wherein the amino acid sequences are free of particles of said virus.

29. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (1) and (2).

30. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (2) and (3).

31. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (3) and (4).

32. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (4) and (5).

33. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (5) and (6).

34. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (6) and (7).

35. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (7) and (8).

36. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (8) and (9).

37. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (9) and (10).

38. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (10) and (11).

39. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (11) and (12).

40. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (12) and (13).

41. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (13) and (14).

42. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (14) and (15).

43. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (15) and (16).

44. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (16) and (17).

45. A composition as claimed in claim 28, wherein the composition consists essentially of the amino acid sequences recited in (17) and (18).

46. An immunogenic composition consisting essentially of a ***peptide*** composition according to claim 28.

47. An immunogenic composition comprising a ***peptide*** composition according to claim 30.

L10 ANSWER 163 OF 163 USPATFULL
88:60690 ***HTLV*** - ***III*** ***envelope*** ***peptides*** .
Heimer, Edgar P., Sparta, NJ, United States
Reddy, Premkumar E., Montclair, NJ, United States
Gallo, Robert C., Bethesda, MD, United States
Wong-Staal, Flossie, Bethesda, MD, United States
Hoffmann-La Roche Inc., Nutley, NJ, United States (U.S. corporation)United States of America, Washington, DC, United States (U.S. government)
US 4772547 19880920
APPLICATION: US 1986-824913 19860203 (6)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present disclosure relates to synthetic ***peptides*** derived from the conserved region of the HTLVIII ***envelope*** proteins. These ***peptides*** are useful as reagents for immunoassays for detection of AIDS antibodies, as components of immunogenic compositions useful as vaccines, and for the production of anti-bodies selective to said ***envelope*** protein and methods for detecting the presence of AIDS antibodies in biological fluid samples.

L10 ANSWER 159 OF 163 USPATFULL
89:71960 Human immunodeficiency virus antigen.
Ivanoff, Lucinda A., Springfield, PA, United States
Petteway, Steven R., Hockessin, DE, United States
E. I. Du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)
US 4861707 19890829
APPLICATION: US 1987-10056 19870202 (7)
DOCUMENT TYPE: Utility.
AB A recombinant ***peptide*** displaying the antigenicity of Human Immunodeficiency Virus (***HIV***) viral antigens is disclosed. The ***peptide*** comprises an antigenic segment having about 150 to about 400 amino acids corresponding to at least about 30 amino acids of the C-terminal of the ***gp120*** domain and at least about 120 amino acids of the N-terminal of the ***gp41*** domain.

L10 ANSWER 156 OF 163 USPATFULL
91:54587 Synthetic vaccine against AIDS virus.
Berzofsky, Jay A., Bethesda, MD, United States
Hale, Paula M., Rockville, MD, United States
Hosmalin, Anne, Bethesda, MD, United States
Margalit, Hanah, Rockville, MD, United States
Spouge, John L., Rockville, MD, United States
Cornette, James L., Ames, IA, United States
The United States of America as represented by the Secretary of the Department of Health and Human Services, Washington, DC, United States (U.S. government)

US 5030449 19910709
APPLICATION: US 1988-222684 19880721 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to ***peptide*** antigens which stimulate helper T lympocytes which specifically recognize ***HIV*** ***envelope*** protein, thereby enhancing antibody production and cytotoxic T cells to inhibit expression of an infection caused by ***HIV*** virus.

L10 ANSWER 151 OF 163 USPATFULL
92:3763 Synthetic ***peptides*** sharing sequence homology with the ***HIV*** ***envelope*** protein.
Berzofsky, Jay A., Bethesda, MD, United States
DeLisi, Charles, Bethesda, MD, United States
Margalit, Hanah, Rockville, MD, United States
Cornette, James L., Ames, IA, United States
Cease, Kemp B., Rockville, MD, United States
Ouyang, Cecilia S., Silver Springs, MD, United States
The United States of America as represented by the Department of Health and Human Services, Washington, DC, United States (U.S. government)
US 5081226 19920114
APPLICATION: US 1990-492318 19900228 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to the identification of short ***peptide*** segments of AIDS virus proteins which elicit T cellular immunity, and to a method of inducing cellular immunity to native proteins of the AIDS virus by immunization with short synthetic ***peptides*** . Five potential ***peptides*** have been identified by searching for regions which can fold as a maximally amphipathic helix. These may be useful to include in either a synthetic ***peptide*** - or recombinant fragment- based vaccine.

L10 ANSWER 145 OF 163 USPATFULL
92:86879 Immunoassays for antibody to human immunodeficiency virus using recombinant antigens.
Luciw, Paul A., Davis, CA, United States
Dina, Dino, San Francisco, CA, United States
Chiron Corporation, Emeryville, CA, United States (U.S. corporation)
US 5156949 19921020
APPLICATION: US 1987-138894 19871224 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Polynucleotide sequences are provided for the diagnosis of the presence of retroviral infection in a human host associated with lymphadenopathy syndrome and/or acquired immune deficiency syndrome, for expression of ***polypeptides*** and use of the ***polypeptides*** to prepare antibodies, where both the ***polypeptides*** and antibodies may be employed as diagnostic reagents or in therapy, e.g., vaccines and passive immunization. The sequences provide detection of the viral infectious agents associated with the indicated syndromes and can be used for expression of antigenic ***polypeptides*** .

L10 ANSWER 140 OF 163 USPATFULL
93:93680 Synthetic ***HIV*** -like ***peptides*** their compositions and uses.
Formoso, Carl, Anhui, China
Olsen, Duane A., Tacoma, WA, United States
Buchanan, Thomas M., Seattle, WA, United States
Immunodiagnostics, Inc., Seattle, WA, United States (U.S. corporation)

US 5260189 19931109
APPLICATION: US 1992-962612 19921015 (7)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Highly immunoreactive regions of ***gp41*** of ***HIV*** -1, gp32 of ***HIV*** -2 and p24 of ***HIV*** -1 were identified using synthetic ***peptides*** . Superior immunoassay performance is obtained with these ***peptides*** linked to carrier proteins as compared to use of the free ***peptides*** . Additional natural and unnatural variants of these reactive regions to define a set of ***peptides*** that, as cysteine-linked ***peptide*** -protein conjugates, provide optimal immunoassay performance including high immunoreactivity with ***HIV*** antibody positive samples, low reactivity with negative samples, high discrimination between positives and negatives, and high specificity. These ***peptide*** conjugates further permit simultaneous detection of ***HIV*** -1 and ***HIV*** -2 antibodies, and make possible rapid and simple test formats that require no instrumentation for detection of these antibodies.

L10 ANSWER 139 OF 163 USPATFULL
94:40195 Expression of HIV1 and HIV2 ***polypeptides*** and their use.
Bayer, Hubert, Weilheim, Germany, Federal Republic of
Kopetzki, Erhard, Penzberg, Germany, Federal Republic of
Boehringer Mannheim GmbH, Mannheim-Waldhof, United States (non-U.S. corporation)
US 5310876 19940510
APPLICATION: US 1991-648796 19910125 (7)
PRIORITY: DE 1990-4002636 19900130
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A fusion protein with at least one antigenic and/or immunogenic determinant from the ***env*** , gag and/or pol region of HIV1 and/or HIV2 which contains the tetrapeptide sequence NH.sub.2 -Met-Tyr-Tyr-Leu as the N-terminal component as well as a process for its production and use.

L10 ANSWER 116 OF 163 USPATFULL
97:36058 ***Peptides*** for ***HIV*** -1 detection.
Bridon, Dominique P., Morton Grove, IL, United States
Sze, deceased, Isaac S.-Y., late of Gurnee, IL, United States by Carolina Luiz, Loch-Hung L. Sze, Leah S. Sze, heirs
Daghfal, David J., Aurora, IL, United States
Jaffe, Keeve D., Trevor, WI, United States
Colpitts, Tracey L., Round Lake, IL, United States
Abbott Laboratories, Abbott Park, IL, United States (U.S. corporation)
US 5624797 19970429
APPLICATION: US 1995-472597 19950607 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB ***HIV*** -1 ***peptides*** having at least one point mutation between position 593 and 611 of the ***HIV*** -1 ***gp160*** amino acid sequence. The point mutation either is at position 604 or 610, or both positions. Immunoassays which utilize these ***peptides*** are provided, as well as, diagnostic test kits which contain these ***peptides*** .

L10 ANSWER 114 OF 163 USPATFULL
97:52100 Tandem synthetic ***HIV*** -1 ***peptides*** .
Sia, Charles D. Y., Thornhill, Canada
Chong, Pele, Richmond Hill, Canada
Klein, Michel H., Willowdale, Canada

Connaught Laboratories Limited, North York, Canada (non-U.S. corporation)
US 5639854 19970617
APPLICATION: US 1994-257528 19940609 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel synthetic ***peptides*** are provided which are candidate vaccines against ***HIV*** -1 and which are useful in diagnostic application. The ***peptides*** comprise an amino acid sequence of a T-cell epitope of the gag protein of ***HIV*** -1, specifically p24E linked directly to an amino acid sequence of a B-cell epitope of the V3 loop protein of an ***HIV*** -1 isolate and containing the sequence GPGR, and/or the ***gp41*** containing the sequence ELKDWA. Multimeric forms of the tandem synthetic ***peptides*** are provided.

L10 ANSWER 109 OF 163 USPATFULL
97:86270 Immunoreactive ***polypeptide*** compositions.
Weiner, Amy J., Benicia, CA, United States
Houghton, Michael, Danville, CA, United States
Chiron Corporation, Emeryville, CA, United States (U.S. corporation)
US 5670152 19970923
APPLICATION: US 1995-440103 19950512 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates generally to immunoreactive ***polypeptide*** compositions comprising hepatitis type C viral epitopes, methods of using the compositions in immunological applications, and materials and methods for making the compositions

L10 ANSWER 108 OF 163 USPATFULL
97:86271 Immunoreactive ***polypeptide*** compositions.
Weiner, Amy J., Benicia, CA, United States
Houghton, Michael, Danville, CA, United States
Chiron Corporation, Emeryville, CA, United States (U.S. corporation)
US 5670153 19970923
APPLICATION: US 1995-440542 19950512 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates generally to immunoreactive ***polypeptide*** compositions comprising hepatitis type C viral epitopes, methods of using the compositions in immunological applications, and materials and methods for making the compositions.

L10 ANSWER 85 OF 163 USPATFULL
1998:58087 ***Peptides*** capable of inducing immune response to ***HIV*** .
Takiguchi, Masafumi, Tokyo, Japan
Miwa, Kiyoshi, Kawasaki, Japan
Ajinomoto Co., Inc., Tokyo, Japan (non-U.S. corporation)
US 5756666 19980526
WO 9511255 19950427
APPLICATION: US 1996-615181 19960404 (8)
WO 1994-JP1756 19941019 19960404 PCT 371 date 19960404 PCT 102(e) date
PRIORITY: JP 1993-261302 19931019
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Herein disclosed is a ***peptide*** which is a fragment of the whole protein of ***HIV*** , the fragment being a ***peptide*** having a sequence of successive 8 to 11 amino acid residues, which corresponds to an HLA-binding motif, which actually binds to HLA and which can induce killer cells capable of attacking ***HIV*** -infected cells as

target cells. The ***peptide*** is effective as an anti-AIDS agent for preventing and curing AIDS.

L10 ANSWER 83 OF 163 USPATFULL
1998:61389 Tandem synthetic ***HIV*** -1 ***peptides*** .
Sia, Charles D. Y., Thornhill, Canada
Chong, Pele, Richmond Hill, Canada
Klein, Michel H., Willowdale, Canada
Connaught Laboratories Limited, North York, Canada (non-U.S. corporation)
US 5759769 19980602
APPLICATION: US 1995-460602 19950602 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel synthetic ***peptides*** are provided which are candidate vaccines against ***HIV*** -1 and which are useful in diagnostic application. The ***peptides*** comprise an amino acid sequence of a T-cell epitope of the gag protein of ***HIV*** -1, specifically p24E linked directly to an amino acid sequence of a B-cell epitope of the V3 loop protein of an ***HIV*** -1 isolate and containing the sequence GPGR, and/or the ***gp41*** containing the sequence ELKDWA. Multimeric forms of the tandem synthetic ***peptides*** are provided.

L10 ANSWER 81 OF 163 USPATFULL
1998:64952 Synthetic ***peptides*** and process of using same for the detection of antibodies to human immunodeficiency virus (***HIV***) ***gp120*** ***envelope*** protein, diagnosis of AIDS and pre-AIDS conditions and as vaccines.
Wang, Chang Yi, Greak Neck, NY, United States
United Biomedical, Inc., Hauppauge, NY, United States (U.S. corporation)
US 5763160 19980609
APPLICATION: US 1995-488252 19950607 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to a method using synthetic ***peptides*** as the solid phase immunoadsorbent for the detection and elicitation of antibodies to Human Immunodeficiency Virus (***HIV***) ***gp120*** , and, in particular, antibodies having ***HIV*** neutralizing capabilities. The amino acid sequences of the ***peptides*** correspond to segments of the external ***envelope*** protein ***gp120*** of ***HIV*** . These ***peptides*** have been found to be highly immunogenic, and are reactive with antibodies in sera of patients with AIDS, ARC or ***HIV*** infected individuals. They can also be used to elicit the production of neutralizing antibodies to ***HIV*** . More specifically, the present invention is directed to the use of a synthetic ***peptide*** selected from the groups consisting of ***peptides*** containing thirty-three amino acids in a prescribed sequence derived from the ***HIV*** - ***gp120*** external protein, analogues, mixtures and poly-L-lysine polymers thereof, for the detection and elicitation of antibodies to ***HIV*** - ***gp120*** . It is particularly useful for the detection and elicitation of antibodies having ***HIV*** neutralizing capabilities. The detection method includes an enzyme linked immunoassay and other forms of immunoassay procedures. The present invention also relates to a method for generating high titer neutralizing antibodies to ***HIV*** ***gp120*** protein in healthy mammals, including humans, by the use of the synthetic ***peptides*** , their analogues or mixtures in either a conjugated or a polymeric form as a key component in a synthetic vaccine for the prevention of AIDS.

L10 ANSWER 56 OF 163 USPATFULL

1998:147041 ***Peptides*** for use in vaccination and induction of neutralizing antibodies against human immunodeficiency virus.
Vahlne, Anders, Hovas, Sweden
Syennerholm, Bo, Goteborg, Sweden
Rymo, Lars, Hovas, Sweden
Jeansson, Stig, Goteborg, Sweden
Horal, Peter, Goteborg, Sweden
Syntello Vaccine Development KB, Gothenburg, Sweden (non-U.S. corporation)
US 5840313 19981124
APPLICATION: US 1995-493235 19950620 (8)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel ***peptides*** are disclosed which correspond to epitopes of the ***HIV*** -1 ***gp120*** protein. These antigenic ***peptides*** induce antibody-dependent cellular cytotoxicity against ***HIV*** , and thus are useful in immunization against ***HIV*** infection and induction of a heightened immune response to ***HIV*** .

L10 ANSWER 15 OF 163 USPATFULL
1999:155899 Mutated proteins encoded by a lentivirus mutated ***env*** gene, ***peptide*** fragments and expression vectors.
Pancino, Gianfranco, Paris, France
Sonigo, Pierre, Paris, France
Centre National De La Recherche Scientifique-CNRS, Paris Cedex, France (non-U.S. corporation)
US 5994516 19991130
WO 9630527 19961003
APPLICATION: US 1997-913953 19971223 (8)
WO 1996-FR449 19960326 19971223 PCT 371 date 19971223 PCT 102(e) date
PRIORITY: FR 1995-3566 19950327
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Mutated proteins coded by a mutated ***env*** gene of a lentivirus, particularly FIV, ***HIV*** or CAEV, ***peptide*** fragments contained in said mutated proteins and expression vectors expressing said mutaded proteins as well as the applications thereof are described. The ***peptide*** fragments are contained in the principal immunodominant domain (PID) of the transmembrane protein (TM) of lentiviruses and particularly of feline immunodeficiency virus (FIV), human immounodeficiency virus (***HIV*** -1 and ***HIV*** -2), arthritis virus and caprine encephalitis virus (CAEV), and are capable of modifying the immunogenic properties of the PID domain and of the ***Env*** protein of the lentiviruses containing them. Such fragments have one of the following sequences: SEQ ID No1: CNQNQWLCK, SEQ ID No2: CNQNQFLCK, SEQ ID No3: CNQNQLWCK, SEQ ID No4: CNQNQPFCK, SEQ ID No5: CEHQHFFCK, SEQ ID No6: CSMGTFFCK, SEQ ID No7: CLTDSFFCK, SEQ ID No8: CELKNFFCK, SEQ ID No9: CRFAAFFCK, SEQ ID No10: ELGCGSKLICKIP, SEQ ID No11: IWGCNQNQFFCTTAVPWN, SEQ ID No12: IWGVAFRQVCTTAVPW.

L10 ANSWER 2 OF 163 USPATFULL
2000:37394 ***HIV*** ***envelope*** ***polypeptides*** .
Berman, Phillip W., Portola Valley, CA, United States
Nakamura, Gerald R., San Francisco, CA, United States
Genentech, Inc., South San Francisco, CA, United States (U.S. corporation)
US 6042836 20000328
APPLICATION: US 1998-134075 19980813 (9)
DOCUMENT TYPE: Utility.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for the rational design and preparation of vaccines based on ***HIV*** ***envelope*** ***polypeptides*** is described. In

one embodiment, the method for making an ***HIV*** ***gp120*** subunit vaccine for a geographic region comprises determining neutralizing epitopes in the V2 and/or C4 domains of ***gp120*** of ***HIV*** isolates from the geographic region and selecting an ***HIV*** strain having ***gp120*** a neutralizing epitope in the V2 or C4 domain which is common among isolates in the geographic region. In a preferred embodiment of the method, neutralizing epitopes for the V2, V3, and C4 domains of ***gp120*** are determined. At least two ***HIV*** isolates having different neutralizing epitopes in the V2, V3, or C4 domain are selected and used to make the vaccine. The invention also provides a multivalent ***HIV*** ***gp120*** subunit vaccine.

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    jj                              kkk        ii
                                     kk
    jj  pp ppp   aaaa   rr rrr   kk  kk  iii    nnnnn
    jj   pp  pp     aa   rrr rr  kk kk    ii    nn  nn
    jj   pp  pp  aaaaa   rr  rr  kkkk     ii    nn  nn
jj  jj   ppppp  aa  aa   rr       kk kk    ii    nn  nn
jj  jj   pp      aaa aa rrrr    kkk  kk  iiii   nn  nn
 jjjj    pppp
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 2222     666    9999
22  22   66     99  99
    22  66      99  99
  222   66666    99999
 22     66  66      99
22  22  66  66     99
222222   6666    999
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5/16/00

L16 ANSWER 340 OF 342 MEDLINE
87080290 Document Number: 87080290. Subregions of a ***conserved*** part of the ***HIV*** ***gp41*** transmembrane protein are differentially recognized by antibodies of infected individuals. Certa U; Bannwarth W; Stuber D; Gentz R; Lanzer M; Le Grice S; Guillot F; Wendler I; Hunsmann G; Bujard H; et al. EMBO JOURNAL, (1986 Nov) 5 (11) 3051-6. Journal code: EMB. ISSN: 0261-4189. Pub. country: ENGLAND: United Kingdom. Language: English.
AB A 240-bp DNA fragment encoding a ***peptide*** , designated ***ENV*** (80), homologous to a ***conserved*** part of the ***gp41*** transmembrane glycoprotein of human immunodeficiency virus (***HIV***) was chemically synthesized and inserted into different plasmid expression vectors. Escherichia coli transformants containing these plasmid constructs produced upon induction high amounts of either an ***ENV*** (80) ***peptide*** of relative molecular mass (Mr) of 10,000 or the same ***ENV*** (80) ***peptide*** N-terminally fused to E. coli chloramphenicol acetyltransferase (CAT) or to mouse dihydrofolate reductase (DHFR) having Mr of 36,000 and 31,000 respectively. All ***polypeptides*** containing the ***ENV*** (80) sequences were strongly reactive with antibodies present in sera from AIDS virus-infected individuals, but not with control sera. The strategy of gene assembly allowed the expression of ***ENV*** (80) subfragments fused to DHFR. The serodiagnosis of 15 positive sera by Western blot analysis using these bacterially synthesized ***ENV*** (80) subfragments revealed the presence of several immunoreactive epitopes on the 80-amino acid ***polypeptide*** which were recognized differently by the various patients.

L16 ANSWER 339 OF 342 MEDLINE
87144025 Document Number: 87144025. A new ELISA test for ***HIV*** antibodies using a bacterially produced viral ***env*** gene product. Schneider J; Wendler I; Guillot F; Hunsmann G; Gallati H; Schoenfeld H J; Stuber D; Mous J. MEDICAL MICROBIOLOGY AND IMMUNOLOGY, (1987) 176 (1) 47-51. Journal code: M58. ISSN: 0300-8584. Pub. country: GERMANY, WEST: Germany, Federal Republic of. Language: English.
AB Screening tests for antibodies to the human immunodeficiency virus (***HIV***), based on the indirect ELISA principle using viral preparations as antigen, yield a substantial number of false-positive and false-negative results. These failures are due to the lack of certain viral ***polypeptides*** or contaminating cellular ***polypeptides*** in viral preparations. Therefore, the accuracy of the screening tests should be improved by using highly purified, synthetic viral antigens. With establishment of such an ELISA antigen in mind, we examined a bacterially synthesized ***polypeptide*** [***ENV*** (80)] that corresponds to 80 ***conserved*** amino acids of the ***HIV*** ***gp41*** transmembrane glycoprotein. ***ENV*** (80) was expressed as a DHFR fusion protein in Escherichia coli. Results obtained by ***HIV*** ELISA and immunoprecipitation with 497 serum samples from various groups at risk of AIDS were compared with those obtained with the ***ENV*** (80) ELISA. The ***ENV*** (80) ELISA was found to be superior to the H9/ ***HTLV*** - ***III*** ELISA with respect to sensitivity and specificity and is almost equivalent in accuracy to immunoprecipitation.

L16 ANSWER 337 OF 342 MEDLINE
87175697 Document Number: 87175697. A ***conserved*** region at the COOH terminus of human immunodeficiency virus ***gp120*** ***envelope*** protein contains an immunodominant epitope. Palker T J; Matthews T J; Clark M E; Cianciolo G J; Randall R R; Langlois A J; White G C; Safai B; Snyderman R; Bolognesi D P; et al. PROCEEDINGS OF THE NATIONAL ACADEMY OF

SCIENCES OF THE UNITED STATES OF AMERICA, (1987 Apr) 84 (8) 2479-83. Journal code: PV3. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB A highly immunogenic epitope from a ***conserved*** COOH-terminal region of the human immunodeficiency virus (***HIV***) ***gp120*** ***envelope*** protein has been identified with antisera from ***HIV*** -seropositive subjects and a synthetic ***peptide*** (SP-22) containing 15 amino acids from this region (Ala-Pro-Thr-Lys-Ala-Lys-Arg-Arg-Val-Val-Gln-Arg-Glu-Lys-Arg). ***Peptide*** SP-22 absorbed up to 100% of anti- ***gp120*** antibody reactivity from select ***HIV*** + patient sera in immunoblot assays and up to 79% of serum anti- ***gp120*** antibody reactivity in competition RIA. In RIA, 45% of ***HIV*** -seropositive subjects had antibodies that bound to ***peptide*** SP-22. Human anti-SP-22 antibodies that bound to and were eluted from an SP-22 affinity column reacted with ***gp120*** in RIA and immunoblot assays but did not neutralize ***HIV*** or inhibit ***HIV*** -induced syncytium formation in vitro, even though these antibodies comprised 70% of all anti- ***gp120*** antibodies in the test serum. In contrast, the remaining 30% of SP-22 nonreactive anti- ***gp120*** antibodies did not react with ***gp120*** in immunoblot assays but did not react in RIA and neutralized ***HIV*** in vitro. Thus, approximately 50% of ***HIV*** -seropositive patients make high titers of nonneutralizing antibodies to an immunodominant antigen on ***gp120*** defined by SP-22. Moreover, the COOH terminus of ***gp120*** contains the major antigen or antigens identified by human anti- ***gp120*** antibodies in immunoblot assays.

L16 ANSWER 332 OF 342 MEDLINE

87252425 Document Number: 87252425. Diagnosis of AIDS by using a 12-amino acid ***peptide*** representing an immunodominant epitope of the human immunodeficiency virus. Gnann J W Jr; Schwimmbeck P L; Nelson J A; Truax A B; Oldstone M B. JOURNAL OF INFECTIOUS DISEASES, (1987 Aug) 156 (2) 261-7. Journal code: IH3. ISSN: 0022-1899. Pub. country: United States. Language: English.

AB We mapped an immunodominant domain of the human immunodeficiency virus (***HIV***). We selected hydrophilic amino acid sequences encoded by ***conserved*** regions of the gag, pol, and ***env*** genes of ***HIV*** as potential antigenic domains. Eighteen ***peptides*** representing these sequences were synthesized; the ***peptides*** elicited strong antibody responses in rabbits. Sera from 53 ***HIV*** -infected patients and 50 controls were tested against the synthetic ***peptides*** . Although no antibodies to ***peptides*** from gag, pol, or ***env*** ***gp120*** proteins were present, antibodies to four of the six ***peptides*** from ***env*** ***gp41*** were detected. Epitope mapping using overlapping ***peptides*** showed that sera from 53 (100%) of 53 ***HIV*** -infected patients (and from none of 50 controls) reacted with ***peptides*** aa584-609 and aa598-609 from ***gp41*** , sera from 32 (60%) of 53 patients reacted with ***peptide*** aa603-614, and sera from 19 (35%) of 53 patients reacted with ***peptides*** aa609-620. Thus, amino acid sequence LeuGlyIleTrpGlyCysSerGlyLysLeuIleCys (aa598-609) from the transmembrane glycoprotein is an immunodominant domain of ***HIV*** recognized by serum antibodies from ***HIV*** -infected patients.

L16 ANSWER 330 OF 342 MEDLINE

87319661 Document Number: 87319661. Synthetic ***peptide*** immunoassay distinguishes ***HIV*** type 1 and ***HIV*** type 2 infections. Gnann J W Jr; McCormick J B; Mitchell S; Nelson J A; Oldstone M B. SCIENCE, (1987 Sep 11) 237 (4820) 1346-9. Journal code: UJ7. ISSN: 0036-8075. Pub. country: United States. Language: English.

AB Efforts to solve the epidemiologic puzzle of AIDS in Africa are

complicated by the presence of multiple human retroviruses. Simple serologic tests that unambiguously distinguish among infections by these retroviruses are essential. To that end, a partially ***conserved*** immunoreactive epitope was identified in the transmembrane glycoproteins of human immunodeficiency viruses (***HIV***) types 1 and 2. Synthetic ***peptides*** derived from these ***conserved*** domains were used in sensitive and specific immunoassays that detect antibodies in sera from patients infected with ***HIV*** -1 or ***HIV*** -2. By making single amino acid substitutions in the ***HIV*** -1 ***peptide*** , it was possible to demonstrate ***HIV*** -1 strain-specific antibody responses to this epitope. Such custom-designed ***peptides*** synthesized from this domain are likely to detect newly discovered ***HIV*** types, define infection with specific ***HIV*** strains, and allow detection of group-common antibodies.

L16 ANSWER 319 OF 342 MEDLINE
89037359 Document Number: 89037359. Epitope mapping of the human immunodeficiency virus type 1 ***gp120*** with monoclonal antibodies. Dowbenko D; Nakamura G; Fennie C; Shimasaki C; Riddle L; Harris R; Gregory T; Lasky L. (Department of Molecular Immunology, Genentech, Inc., South San Francisco, California 94080.) JOURNAL OF VIROLOGY, (1988 Dec) 62 (12) 4703-11. Journal code: KCV. ISSN: 0022-538X. Pub. country: United States. Language: English.
AB A soluble form of recombinant ***gp120*** of human immunodeficiency virus type 1 was used as an immunogen for production of murine monoclonal antibodies. These monoclonal antibodies were characterized for their ability to block the interaction between ***gp120*** and the acquired immunodeficiency syndrome virus receptor, CD4. Three of the monoclonal antibodies were found to inhibit this interaction, whereas the other antibodies were found to be ineffective at blocking binding. The ***gp120*** epitopes which are recognized by these monoclonal antibodies were mapped by using a combination of Western blot (immunoblot) analysis of ***gp120*** proteolytic fragments, immunoaffinity purification of fragments of ***gp120*** , and antibody screening of a random ***gp120*** gene fragment expression library produced in the lambda gt11 expression system. Two monoclonal antibodies which blocked ***gp120*** -CD4 interaction were found to map to adjacent sites in the carboxy-terminal region of the glycoprotein, suggesting that this area is important in the interaction between ***gp120*** and CD4. One nonblocking antibody was found to map to a position that was C terminal to this CD4 blocking region. Interestingly, the other nonblocking monoclonal antibodies were found to map either to a highly ***conserved*** region in the central part of the ***gp120*** ***polypeptide*** or to a highly ***conserved*** region near the N terminus of the glycoprotein. N-terminal deletion mutants of the soluble ***envelope*** glycoprotein which lack these highly ***conserved*** domains but maintain the C-terminal CD4 interaction sites were unable to bind tightly to the CD4 receptor. These results suggest that although the N-terminal and central ***conserved*** domains of intact ***gp120*** do not appear to be directly required for CD4 binding, they may contain information that allows other parts of the molecule to form the appropriate structure for CD4 interaction.

L16 ANSWER 316 OF 342 MEDLINE
89141403 Document Number: 89141403. Use of synthetic oligopeptides in identification and characterization of immunological functions in the amino acid sequence of the ***envelope*** protein of ***HIV*** -1. Modrow S; Hoflacher B; Mellert W; Erfle V; Wahren B; Wolf H. (Max von Pettenkofer-Institut, Ludwig-Maximilians-Universitat, Munchen, F.R.G.) JOURNAL OF ACQUIRED IMMUNE DEFICIENCY SYNDROMES, (1989) 2 (1) 21-7. Journal code: JOF. ISSN: 0894-9255. Pub. country: United States. Language:

English.
AB Following computer-assisted analysis of the amino acid sequence of various ***HIV*** -1 isolates, we synthesized a series of oligopeptides derived from variable and ***conserved*** regions of the ***envelope*** protein complex ***gp120*** / ***gp41*** . The ***peptides*** were used in ELISA tests for their reactivity with human antisera from ***HIV*** -1 positive individuals; patients with clinically manifested AIDS showed only a rather limited reaction, predominantly with two ***peptides*** (p102-112, p316-326), which is in contrast to sera from ***HIV*** -1 positive asymptomatic individuals, whose sera were reactive with almost all ***peptides*** . Using consecutive sera of the same patients, decreasing antibody titers to defined epitopes could be shown to occur during the development of AIDS. Cellular immune response recognition was analyzed in T-cell proliferation assays by [3H]thymidine incorporation. One ***peptide*** localized in a ***conserved*** region clearly induced proliferation of T-cells. Those data were combined to a map of the functions localized in the various regions of the ***HIV*** -1 ***envelope*** proteins.

L16 ANSWER 312 OF 342 MEDLINE
89303784 Document Number: 89303784. Identification of nanopeptide from ***HTLV*** - ***III*** , ***ARV*** -2 and LAVBRU ***envelope*** ***gp120*** determining binding to T4 cell surface protein. Veljkovic V; Metlas R. (Laboratory for Multidisciplinary Research RA 180/2, Boris Kidric Institute, Beograd, Yugoslavia.) CANCER BIOCHEMISTRY BIOPHYSICS, (1988 Nov) 10 (2) 91-106. Journal code: CL0. ISSN: 0305-7232. Pub. country: ENGLAND: United Kingdom. Language: English.
AB The information contained in the primary structure of ***HIV*** ***envelope*** ***gp120*** determining its biological activity, was analyzed by the use of the informational spectrum method. The parameter determining the interaction between ***gp120*** and T4 cell-surface protein was defined. On the basis of this data in the ***conserved*** region of ***gp120*** from ***HTLV*** - ***III*** , LAVBRU and ***ARV*** -2, a nanopeptide NAKTIIVQL was identified as a potential binding domain which could be used as a component of an effective therapeutic agent or as a vaccine component.

L16 ANSWER 309 OF 342 MEDLINE
89352112 Document Number: 89352112. Accessibility of the highly ***conserved*** amino- and carboxy-terminal regions from ***HIV*** -1 external ***envelope*** glycoproteins. Bahraoui E; Clerget-Raslain B; Granier C; Van Rietschoten J; Sabatier J M; Labbe-Julie C; Ceard B; Rochat H; Gluckman J C; Montagnier L. (Unite d'Oncologie Virale, Institut Pasteur, Paris, France..) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1989 Aug) 5 (4) 451-63. Journal code: ART. ISSN: 0889-2229. Pub. country: United States. Language: English.
AB Amino- and carboxy-terminal extremities of the ***envelope*** external glycoproteins are regions that have remained highly ***conserved*** between human immunodeficiency viruses ***HIV*** -1 and ***HIV*** -2. The corresponding ***peptides*** have been synthesized and their structure and function analyzed. Circular dichroism spectra showed evidence of alpha helical conformation when the ***peptides*** were dissolved in the nonpolar solvent trifuoroethanol. These two regions are indeed exposed on the molecule because they were accessible to their respective specific antibodies on the native ***gp160*** precursor or processed ***gp120*** glycoproteins of ***HIV*** -1. Neither the ***peptides*** nor rabbit or human antibodies directed against the N- and C-terminal ***peptides*** interfered with the interaction between ***HIV*** -1 external glycoprotein ***gp120*** and its CD4 cellular receptor. Taken together, these results indicate that N- and C-terminal regions of ***gp120*** are accessible on the quaternary structure of

the virion as well as on the soluble form of ***gp120*** and that these regions are not directly or indirectly involved in the binding of ***gp120*** to CD4.

L16 ANSWER 308 OF 342 MEDLINE
89367330 Document Number: 89367330. Principal neutralizing domain of the human immunodeficiency virus type 1 ***envelope*** protein. Javaherian K; Langlois A J; McDanal C; Ross K L; Eckler L I; Jellis C L; Profy A T; Rusche J R; Bolognesi D P; Putney S D; et al. (Repligen Corporation, Cambridge, MA 02139.) PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1989 Sep) 86 (17) 6768-72. Journal code: PV3. ISSN: 0027-8424. Pub. country: United States. Language: English.
AB The principal neutralizing determinant of human immunodeficiency virus type 1 (***HIV*** -1) is located in the external ***envelope*** protein, ***gp120*** , and has previously been mapped to a 24-amino acid-long sequence (denoted RP135). We show here that deletion of this sequence renders the ***envelope*** unable to elicit neutralizing antibodies. In addition, using synthetic ***peptide*** fragments of RP135, we have mapped the neutralizing determinant to 8 amino acids and found that a ***peptide*** of this size elicits neutralizing antibodies. This sequence contains a central Gly-Pro-Gly that is generally ***conserved*** between different ***HIV*** -1 isolates and is flanked by amino acids that differ from isolate to isolate. Antibodies elicited by ***peptides*** from one isolate do not neutralize two different isolates, and a hybrid ***peptide*** , consisting of amino acid sequences from two isolates, elicits neutralizing antibodies to both isolates. By using a mixture of ***peptides*** of this domain or a mixture of such hybrid ***peptides*** the type-specificity of the neutralizing antibody response to this determinant can perhaps be overcome.

L16 ANSWER 304 OF 342 MEDLINE
90197991 Document Number: 90197991. Use of a ***conserved*** immunodominant epitope of ***HIV*** surface glycoprotein ***gp41*** in the detection of early antibodies. Cumming S A; McPhee D A; Maskill W J; Kemp B E; Doherty R R; Gust I D. (NH & MRC Special Unit for AIDS Virology, Macfarlane Burnet Centre for Medical Research, Fairfield Hospital, Victoria, Australia..) AIDS, (1990 Jan) 4 (1) 83-6. Journal code: AID. ISSN: 0269-9370. Pub. country: United States. Language: English.
AB An enzyme immunoassay (EIA) utilizing a synthetic ***peptide*** analogue of ***HIV*** ***gp41*** (amino acids 579-599, RILAVERYLKDQQLLGIWGCS) as antigen was compared with two commercial assays (Genetic Systems, Abbott ENVACORE) for the ability to detect antibodies in the early stages of infection. Two panels, consisting of 96 sera from 15 people and 140 sera from 44 people seroconverting to ***HIV*** , were examined. In the first group the synthetic ***peptide*** assay (***gp41*** EIA) detected antibodies before the Genetic Systems EIA in seven out of 15 people and concurrently in the remaining eight. With the second panel the Abbott ENVACORE assay detected antibodies before the ***gp41*** EIA in two out of 44 people while the ***gp41*** EIA detected antibodies first in six out of 44. In the remaining 36 people antibodies were detected simultaneously by the two tests. The ***gp41*** EIA usually detected anti- ***HIV*** antibodies before or concurrently with the two commercial assays examined suggesting that the epitope cluster represented by this ***peptide*** is recognized early in infection.

L16 ANSWER 301 OF 342 MEDLINE
90347803 Document Number: 90347803. Analysis of a highly immunodominant epitope in the human immunodeficiency virus type 1 transmembrane

glycoprotein, ***gp41*** , defined by a human monoclonal antibody. Bugge T H; Lindhardt B O; Hansen L L; Kusk P; Hulgaard E; Holmback K; Klasse P J; Zeuthen J; Ulrich K. (Laboratory of Tumor Virology, Fibiger Institute, Danish Cancer Society, Copenhagen.) JOURNAL OF VIROLOGY, (1990 Sep) 64 (9) 4123-9. Journal code: KCV. ISSN: 0022-538X. Pub. country: United States. Language: English.

AB A human monoclonal antibody, 41-7 [immunoglobulin G1(kappa)], directed against the transmembrane glycoprotein ***gp41*** of the human immunodeficiency virus type 1 (***HIV*** -1) has been produced by direct fusion of lymph node cells from an ***HIV*** -1-infected individual with a human B-lymphoblastoid cell line. The minimal essential epitope for 41-7 was mapped to a ***conserved*** seven-amino acid sequence, N-CSGKLIC-C, located within the N-terminal part of ***gp41*** . Antibodies blocking the binding of 41-7 could be detected in the serum of all ***HIV*** -1-infected individuals tested, irrespective of the stage of the infection. The epitope is located externally to the plasma membrane, and it is accessible to antibody in the native conformation of the glycoprotein. Despite this, no neutralizing activity of 41-7 could be demonstrated in vitro. These data indicate, directly and indirectly, that this immunodominant epitope on ***gp41*** , although exposed on the viral surface, elicits antibodies lacking antiviral activity and, hence, should be avoided in future vaccine candidates.

L16 ANSWER 300 OF 342 MEDLINE

90351568 Document Number: 90351568. Immunogenicity and antigenicity of ***conserved*** ***peptides*** from the ***envelope*** of ***HIV*** -1 expressed at the surface of recombinant bacteria. Charbit A; Molla A; Ronco J; Clement J M; Favier V; Bahraoui E M; Montagnier L; Leguern A; Hofnung M. (Unite de Programmation Moleculaire et Toxicologie Genetique (CNRS UA271, INSERM U163), Paris, France.) AIDS, (1990 Jun) 4 (6) 545-51. Journal code: AID. ISSN: 0269-9370. Pub. country: United States. Language: English.

AB We expressed ***peptides*** from the ***HIV*** -1 ***envelope*** protein at the surface of Escherichia coli by genetic insertions into an exposed loop of the outer membrane protein LamB. Recombinant bacteria expressing eight ***peptides*** from gp110 (pep1-pep8), ***conserved*** between ***HIV*** -1 and ***HIV*** -2, were used as live immunogens in rabbits by the intravenous route. The eight constructions elicited anti-LamB antibodies, showing that the hybrid proteins were immunogenic. One of them, LamB-pep8, gave rise to antibodies able to react with ***gp160*** and to neutralize ***HIV*** -1 in vitro. We also show that this type of recombinant E. coli can provide a convenient reagent to monitor and characterize specific antibodies. Recombinant clones were used to test sera of seropositive individuals, as well as to narrow down the monoclonal antibody 110-1 recognition site to a cluster of eight residues at the carboxy-terminal end of gp110.

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    jj                              kkk        ii
                                    kk
    jj  pp ppp    aaaa    rr rrr    kk  kk  iii     nnnnn
    jj   pp  pp      aa    rrr rr   kk kk    ii     nn  nn
    jj   pp  pp   aaaaa    rr  rr   kkkk     ii     nn  nn
jj  jj   pppppp  aa  aa    rr       kk kk    ii     nn  nn
jj  jj   pp       aaa aa rrrr     kkk  kk  iiii    nn  nn
 jjjj    pppp
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  222       77  00 0000
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22  22     77   000  00
222222     77    00000
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                E SONIGO PIERRE/IN
L2           20 S E3
L3            2 S L2 NOT L1
                E WAIN-HOBSON SIMON/IN
                E WAIN HOBSON SIMON/IN
L4           10 S E3
L5            4 S L4 NOT L1 OR L3
                E MONTAGNIER LUC/IN
L6           55 S E3
L7           36 S L6 NOT (L1 OR L2 OR L4)
L8         8841 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L9         2003 S L8 AND (VARIANT?)
L10        1183 S L9 AND (NUCLEOTIDE SEQUENCE?)
L11          41 S L10 AND (MOLECULAR CLONE?)

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                E SONGIO P/IN
                E SONIGO/IN
L13           4 S E3
                E WAIN-HOBSON/IN
L14          15 S E2
                E WAINHOBSON/IN
                E HOBSON/IN
L15          24 S E3
                E MONTAGNIER/IN
L16          30 S E3
L17        1819 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L18         437 S L17 AND (VARIANT?)
L19         246 S L18 AND (NUCLEOTIDE SEQUENC?)
L20         190 S L19 AND (MOLECULAR CLON?)

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L22          59 S E3
L23          52 S L22 NOT L21
                E WAIN-HOBSON S/AU
                E WAIN HOBSON S/AU
L24         102 S E3
L25          93 S L24 NOT (L21 OR L22)
                E MONTAGNIER LUC/AU
L26         309 S E1
L27         296 S L26 NOT (L21 OR L22 OR L24)
L28       39108 S (HIV-1 OR HUMAN IMMUNODEFICIENCY VIRUS TYPE 1)
L29        1600 S L28 AND VARIANT?
L30          66 S L29 AND (NUCLEOTIDE SEQUENC?)
L31           9 S L30 AND (MOLECULAR CLON?)
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